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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                         No
  987654921
                                                                                                                                                                                                                                                                                  pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                         Score
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158.727 Million cell updates/sec
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376
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Copyright (c) 1993 - 2003 Compugen Ltd
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SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
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863
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AAB92688
AAM93444
AAB94104
AAB95317
AAB953139
                      ABG04066
AAW64221
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      Human protein sequ
Human protein sequ
Novel human diagno
Human secreted pro
Human CJ145_1 pro
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                                                                                                         Human
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polypeptide,
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AAM26950	AAM14533	AAM66665	AAM54270	ABB18950	ABB33490	ABB28314	ABG48336	ABG20886	ABG20323	ABG22456	AAM79330	AAM79329	AAM78345	AAY55935	AAM78346	ABB71451	ABB60133	AAU46062	ABB68321	ABB66233	ABB93287	ABP69529	ABB57260	AAM52303	AAM52309	ABG74448	ABG70177	ABG/91/3				7 7 7	9420	/146	
	400	#067	DEGETT CAPTO	2 45 ± 117	# 4 0 4 0	100#		liman	I human	T uman	n procer	Human protein sex	=	Human KHSZ procern	Human protein sev	Drosophila meranog	Drosophila meranog	Propionibacterium	Drosophila meranog	Drosophila melanog	Herbicidally activ	Human polypeptide	Mouse ischaemic co		zyxine fr	erminal c	semap	acid sequen	semaphori	semaphorin	-2, In	Ylod Iddw	protein seg	protein seq	Human semaphorin 6

ALIGNMENTS

AAY71461 standard; peptide; 72

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AAY71461;

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RESULT 1
AAY71461
ID AAY7
XX
AC AAY
XX
DT 04-
DT 04-
XX
KW Hu
KW Hu
KW Hu
KW Ge
KW G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding domain of human semaphorin 6A-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000 (first entry)
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                           02-JUN-2000
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                                                                                                                  26-NOV-1998;
                                                                                                                                                                                                                                    26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200031252-A1
                                                                                                                                   98EP-0122441
                                                                                                                                                                                                                                          99WO-EP09215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
51..56
/note= "Specific binding motif for members of Ena/VASP protein family, especially Evl"
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RESULT 2
AAB92688
ID AAB9
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human semaphorin 6A-1 (!HAA)SEMA6A-1) which is involved in neuronal development and regeneration mechanisms during apoptosis. The binding domain shows homology to Zyxin protein and selectively binds to members of EnaryMaSP protein family, especially EVI. (HSA)SEMA6A-1 is a member of protein family, displaying secreted or transmembrane-based repulsive guidance cues critically involved in neuronal development. Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and moderate in lung. The present sequence is useful as diagnostic and therapeutic agents, for modulating the immune system, in gene therapy, for effecting differentiation, cytoskeletal stabilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent, therapeutic agent, for modulating immune system, in gene therapy or for effecting differentiation, cytoskeletal stabilization and/or plasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Behl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAD01234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 22; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and plasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a binding domain of transmembranous
                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                             AAB92688 standard;
                                                                                                                                                                                                                                                                                     Human; primer;
                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:11073.
                                                                                                                                                                                                                                                                                                                                            26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                   AAB92688;
                                                                                                                                                                                                              07-FEB-2001.
                                                                                                                                                                                                                                      EP1074617-A2
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                   28-JUL-2000; 2000EP-0116126
                                                                           (HELI-) HELIX RES
                                                                                                       09-JUN-2000;
               WPI; 2001-318749/34
                                       Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-400065/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klostermann
                                                     Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 60
                                      sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                           99JP-0248036
                                                                               INST
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                                                                                                                                                                                                                                                                                                                                                                                                 507
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                                          Hayashi K, i
A, Nagai K,
                                             Saito K,
(, Otsuki
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                                                            Yamamoto
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#####XX2020202020202020202020202020
                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                full-length cDNAs
                                                                                                                                                                                                                   detection
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Claim 8; SEQ ID 11073; 2537pp + CD ROM; English

The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligo-dr primer and an oligonucleotide complementary ct to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the cc oligonucleotide comprises at least 15 nucleotides; or (b) a combination cc of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end cc polynucleotide which comprises a 3'-end sequence complementary to a sequence and an oligonucleotide comprising a sequence complementary to a combination of cc polynucleotide which comprises a 3'-end sequence where the cc oligonucleotide comprises a 3'-end sequence where the specification. The primers sets can be used in antisense therapy and the specification. The primers sets can be used in antisense therapy and cc particularly full-length cDNAs. The primers are also useful for the primers are also useful for the comprise of the abnormality of the proteins encoded by detection and/or diagnosis of the abnormality of the proteins encoded by cDNAs easily without any specialised methods. AAH03166 to AAH13628 and can also useful oligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification of confidence of the protest oligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification of the present invention.

밁 Ωy 20 밁 Matches Query Match Sequence Local 436 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 496 LSTSMKPNDACT 61 LSTSMKPNDACT 72 1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP Similarity Conservative 100.0%; 100.0%; 0; Score 376; DB 22; Pred. No. 8.3e-34; ; Mismatches 0; Length 507; Indels 0; 495 60

0;

507 AA;

AAM93444

AAM934444

AAM93444

AAM9

AAC AAM9

XX AAM9

XX Humm

XX Humm

XX Humm

XX Humm

XX EP1

PN 05
XX 08
PF 07
PF 07
PF 07
PF 11
PR RESULT 3 Human; full length cDNA; cDNA synthesis; oligo-capping. Human polypeptide, SEQ ID NO: 06-NOV-2001 AAM93444; AAM93444 standard; 08-JUL-1999; 11-JAN-2000; 07-JUL-2000; 2000EP-0114089 05-SEP-2001 EP1130094-A2 02-MAY-2000; (HELI-) HELIX RES INST Nishikawa T, Isogai T, tsu A, Sugiyama T, Nagai ; 99JP-0194486. ; 2000JP-0118774. ; 2000JP-0183765. (first entry) Protein; 562 AA. 3088 Hayashi K, K, Kojima Ś Ishii S,

Wakamatsu A,

Otsuki T,

Kawai Y;

Koga H;

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Вþ
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules have been determined. Primers for synthesising the full length CDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ciones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to primers for synthesising full length clones. 830 cDNA molecules encoding a human protein have been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830 Primers useful for synthesizing full length cDNA clones and their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94104 standard; Protein; 562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Human protein sequence SEQ ID NO:14328
                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2001 (first entry)
                                                                                                                                                                           11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                                                                                                                                              07-FEB-2001
                                                                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                 Human; primer;
Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                          WPI; 2001-318749/34.
                                                                                                                                                             09-JUN-2000;
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                                                                                                                               (HELI-)
                                                                                                                                                                                                        27-AUG-1999;
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                                                                                                                                  HELIX RES INST.
                                                                                                      Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3088; 1380pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPPAPORVDSIQVHSSOPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSTSMKPNDACT 562
                                                                                       Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 AA;
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; 2000JP-0183767.
; 2000JP-0241899.
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                                                                                                                                                                                                        99JP-0248036.
99JP-0300253.
                                                                                       Nishikawa T,
T, Wakamatsu
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Pred. No. 9.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RRESULT 5
AAB9517
IID AAB99
XX AAB9517
AC AAB9
XX AAB9517
AC AAB9
XX Huma
XX Huma
XX Huma
XX EP11
XX E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ct the 5602 nucleotide sequences defined in the specification, where the configuration comprises at least 15 nucleotides; or (b) a combination coff an oligonucleotide comprises a polynucleotide which comprises a 5 - end complementary strand of a polynucleotide which comprises a 5 - end coligonucleotide which comprises a 3 - end sequence complementary to a coligonucleotide which comprises a 3 - end sequence complementary to a coligonucleotide comprises a 3 - end sequence, where the combination of the 5 - end sequence/3 - end sequence is selected from those defined in coligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primers sets can be used in antisense therapy and coligonucleotide comprises a treat of the specification of coligonucleotides. The primers are useful for synthesising polynucleotides, coligonucleotides of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cannot coligonucleotides, all of which are used in the exemplification represent oligonucleotides, all of which are used in the exemplification of coligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 14328; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       full-length cDNAs
                                                                                                                                                                                                                29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                   Ota T,
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human protein sequence SEQ ID NO:17568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB95317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB95317 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126
                                                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PPPAPQRVDSTQVHSSQPSGQAVTVSRQPSLNAVNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                   Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPAPQRVDSTQVHSSQPSGQAVTVSRQPSLNAXNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSTSMKPNDACT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSTSMKPNDACT 72
                                sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                   99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                             2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 376; DB 22;
Pred. No. 9.4e-34;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑA
                                         Hayashi K,
A, Nagai K,
                                                                         Saito K,
                                                   Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                   Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       550
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RESULT 6
AAB919
ID AAB9
XX AAB919
XX AAB9
XX AAB9
DT 26-J
DT 26-J
CT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΔÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary to the comprises and an oligonucleotide comprises a greence complementary to a complementary for a comprise and the comprises at least 15 nucleotides and the combination of comprises at least 15 nucleotides and the combination of complementary. The primer sets can be used in antisense therapy and complementary full-length cDNAs. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the comprise complementary of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CAAH35633 to AAH18742 represent human cDNA sequences; AAAB92446 to compresent oligonucleotides, all of which are used in the exemplification complementary to the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                             28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                            07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB95139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB95139 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAVNSLTRSGLKRTPSLKPDVPPKPSFAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID 17568; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSTSMKPNDACT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention describes primer sets for synthesising 5602 cDNAs defined in the specification. Where a primer set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                 99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence SEQ ID NO:17154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                 99JP-0248036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 376; DB 22; Pred. No. 9.7e-34; Nismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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13-FEB-2002

(first entry)

Novel human diagnostic protein #4057

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

supplement;

30-MAR-2001; 2001WO-US08631

11-0CT-2001 WO200175067-A2

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The present invention describes primer sets for synthesising 5602 cc full-length cDNAs defined in the specification. Where a primer set cc comprises: (a) an oligoroff primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the colligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence where the component of the primerses as 3'-end sequence, where the component of the specification. The primers sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and comparise therapy and the specification. The primer sets can be used in antisense therapy and comparise therapy and the specification of 
QΨ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 17154; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                     ABG04066 standard; Protein; 863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSTSMKPNDACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 72; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSTSMKPNDACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 376; DB 22;
Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K,
A, Nagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K, Y
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 699;
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60 0

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RESULT 8
AAW64221
ID AAW6
XX AAW6
AC AAW6
XX Huma
DT 06-0
XX
DE Huma
XX Secr
KW celll
KW regu
KW chem
KW chem
KW chem
KW chem
KW chem
KW chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                                                                                                                                                                         Βb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG00377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the product of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, Oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                            Secreted protein; human fetal brain; nutrition; cytokine; stimulant; cell proliferation; differentiation; immune system; suppressor; ligand; regulator; hematopolesis; tissue growth; activin; inhibin; haemostatic; chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
                                                                            anti-inflammatory.
                                                                                                                                                                                          Human secreted protein from clone CJ145_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                      Homo sapiens
                                                                                                                                                                                                                                                                                                           AAW64221 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 792 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 851
                                                                                                                                                                                                                                                                                                                                                                                                           852 LSTSMKPNDACT 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; SEQ ID No 34425; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          863 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                               974 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 376; DB 22;
Pred. No. 1.6e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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WO9827205-A2

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RESULT 9
AAB 9731
ID AAB
XX
AAB 0731
AC AAB
XX
O7-
XX
O7-
XX
Hum
DE Hum
KW dif
KW hae
KW hae
XX
Hom
OS Hom
OS Hom
OS 100
DY 14-
PF 14-
PF 14-
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                                                                                                                                                                                                                                                                                                                                                                                                                    B
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a novel secreted protein from clone CJ145_1 isolated from a human fetal brain cDNA library. This protein has applications for nutritional use, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombotic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity and other activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides and secreted proteins - obtained from human foetal brain, human adult testes, human adult brain and human adult salivary gland cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17j; Page 71-74; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV44295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1997;
18-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-1998
                                                                                                                                                          Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                             07-JUN-2001
                                                                                                                                                                                                                                                                                                AAB90731 standard; Protein;
               17-SEP-1999;
                                       14-SEP-2000; 2000WO-US25135
                                                                                             WO200119988-A1
                                                                  22-MAR-2001
                                                                                                                                               haematopoiesis
                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998-362774/31.
                                                                                                                                                                                                                                                                                                                                                                    963 LSTSMKPNDACT 974
                                                                                                                                                                                                                                                                                                                                                                                                                    903 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                           61 LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PPPAPORVDSIQVHSSOPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                CJ145_1 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                974 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0991872.
96US-0769192.
97US-0783401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-US23330
               99US-0398829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     < ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lavallie ER, Treacy M;
                                                                                                                                                                                                                                                                                                   975 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 376; DB 19;
Pred. No. 1.9e-33;
                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  мссоу лм,
                                                                                                                                                                                                                      161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,:
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60 962

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AAY71460
ID AAY71
XX AY71
XX AY71
XX AY71
XX U4-OC
DT 04-OC
XX Human
XX Human
KW neuro
KW gene
KW cytos
XX Homo
XX Homo
FFT Bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haematopoiesis regulating activity; tissue growth activity; activit/inibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAB90667 - AAB90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haematopoiesis activity; cadherin/tumour suppressor activity; an tumour inhibition activity. Included in the invention are probes represented in Ansy8572 which are specific for the cD encoding the secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF98469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-244801/25.
                                                                                                                                                                                                                                 neuronal regeneration; Ena/VASP protein family; immunomodulatory; gene therapy; diagnostic agent; therapeutic agent; differentiation; cytoskeletal stabilisation; plasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71460 standard; Protein; 1030 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 487-490; 557pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids encoding polypeptides, useful for modulating e.g. cytokine and cell proliferation/differentiation activity, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs K,
                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                        Human semaphorin 6A-1.
                                                                                                                                                                                                                                                                                                                                                                                           AAY71460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system and hematopoiesis regulating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST
                                                 Binding-site
                                                                                                                                                    Binding-site
                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                        Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;
                                                                                                                                                                                                                                                                                                                                                         04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSTSMKPNDACT 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 975 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                             Ena/VASP p
1009..1014
                                                                                                  /note= "Zyxin-like domain that selectively binds to members of Ena/VASP protein family, especially Evl" 957..961
                                                                                                                                                  Location/Qualifiers 959..1030
                 Ena/VASP protein family,
                            /note= "Specific binding motif for members of
                                                                                    /note= *Specific binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaVallie ER,
Bowman MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC
                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 376; DB 22;
Pred. No. 1.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                   family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins-Racie LA,
Spaulding V, Agosi
                 especially Evl'
                                                                                  motif for members
                                                                   especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                    Evl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
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RESULT 11
AAB94239
ID AAB94239
AC AAB94
AC AAB94
AC BAB94
XX 26-JU
DT 26-JU
XX Humar
XX Humar
XX Humar
XX Homo
XX Homo
XX EP10;
YX 28-JU
YR 29-JU

Human; primer;

detection; diagnosis; antisense therapy; gene therapy.

sapiens

29-JUL-1999;

99JP-0248036

28-JUL-2000; 2000EP-0116126

07-FEB-2001 EP1074617-A2 Human protein sequence

SEQ

ID NO:14623

밁

1019 LSTSMKPNDACT 1030

1018 60

AAB94239 standard;

Protein;

451

AA

AAB94239

26-JUN-2001

(first entry)

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QΨ
                                      밁
                                                                                                                                                                              Qγ
                                                                                                                           Query Match
Best Local :
                                                                                                            Matches
                                                                                                                                                                                                                        regeneration mechanisms during apoptosis. Semaphorin is a family of proteins displaying secreted or transmembrane-based repulsive guidance cues critically involved in neuronal development. The present sequence was isolated from human 1-ZAP Express cDNA library which was screened using a PCR fragment amplified from human neuroblastoma cell line SK-N-MC cDNA. The (HSA)SEMA6A-1 protein contains a Zyxin-like domain that selectively binds to members of Ena/VASP protein family especially EVI. Expression of (HSA)SEMA6A-1 is highest in embryonic brain and kidney and moderate in lung. The present sequence is useful as diagnostic and therapeutic agents, for modulating the immune system, in gene therapy, for effecting differentiation, cytoskeletal stabilisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent, therapeutic agent, for modulating immune system, in gene therapy or for effecting differentiation, cytoskeletal stabilization and/or plasticity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W0200031252-A1.
                                                                                                                                                                              Sequence
                                                                                                                                                                                                             and plasticity.
                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a transmembranous human semaphorin 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal develops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 29-33; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAD01233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Behl C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-400065/34.
                                    959 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
   61 LSTSMKPNDACT 72
                                                                                                        72;
                                                       1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPFKPSFAP
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klostermann
                                                                                                                                                                              1030 AA;
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98EP-0122441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-EP09215
                                                                                                                           100.0%;
                                                                                                            0;
                                                                                                                           Score 376; DB 2
Pred. No. 2e-33;
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             neuronal development and
                                                                                                                                           21;
                                                                                                            0;
                                                                                                                                             Length 1030;
                                                                                                              Indels
                                                                                                              0;
                                                                                                            Gaps
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RESULT 12
AAB94296
ID BAB94
XX AAB94
AC AAB94
XX 26-JI
XX Huma,
XX Huma,
XX Huma
XX Homo
OS Homo
XX EP1(
XX EP1(
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotide comprises at least 15 nucleotides and the combination of the 5'cend sequence/3'end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH31633 to AAH18742 represent human cDNA sequences; AAB92446 to AAH18742 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detecti and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 14623; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                      EP1074617-A2
                                                                                        Human; primer;
                                                                                                                           Human protein sequence SEQ ID NO:14749.
                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                                   AAB94296 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention describes primer sets for synthesising 5602
                                                                                                                                                                                                                                                                                                                                                                                        380 PTPTGAKVDYIQ-----GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP
                                                                                                                                                                                                                                                                                                                                                       55 KPSFAPLSTSMKP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-
                                                                                                                                                                                                                                                                                                                        KPSFVPQTPSVRP 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                              (first entry)
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                                                                                           detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the specification. Where a primer set r primer and an oligonucleotide complementary
                                                                                           diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 163.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           --RSGLKRTPSLKPDVPP 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
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RESULT 13
ABU11724
ID ABU117
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AC ABU11
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MDDT;
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB02446 to AAB35893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 14749; 2537pp + CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention.
                                Human MDDT polypeptide SEQ ID 671.
                                                                                                                                      ABU11724 standard; Protein; 474 AA
MDDT; human; disease detection and treatment molecule polypeptide;
                                                                    13-FEB-2003
                                                                                                                                                                                                                                                                                             393
                                                                                                                                                                                                                                                           55 KPSFAPLSTSMKP 67
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                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                           KPSFVPQTPSVRP 458
                                                                                                                                                                                                                                                                                            PTPTGAKVDYIQ-----
                                                                                                                                                                                                                                                                                                                          PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 464 AA;
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                              43.5%;
50.7%;
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                                                                                                                                                                                                                                                                                            GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    т,
                                                                                                                                                                                                                                                                                                                                                                                Score 163.5; DB : Pred. No. 6.1e-10;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
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456 KPSFVPQTPSVRP 468

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Query Match
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                                                                                                                                                                                                                                                                                                               antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, proliferative disorders (e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABUI1450-ABUI1845 represent the MDDT polynucleotides encoded by ABUI1845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; ceal proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia; psoriasis; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 671; 339pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Datto A,
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17-MAY-2001;
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29-MAR-2001;
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                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                  403
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55 KPSFAPLSTSMKP 67
                                                                                                                                                                         Similarity
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                                               PTPTGAKVDYIQ----
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H, David MH, Lewis SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marwaha R,
                                                                                                                                                                                                                                                474 AA;
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2001US-300001P
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2001US-299428P.
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2001US-291829P.
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2001US-280068P.
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50.7%;
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                                                  --GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP
                                                                                                                                                 8
                                                                                                                                              Score 163.5; DB 2
Pred. No. 6.3e-10;
8; Mismatches 15
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A, Chen
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, Kleefeld '
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Harris B;
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RESULT 14
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/note= "Identified by HMMER-PFAM"
67.182
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381
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283
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/note= "Identified by BLAST-PRODOM"
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'Identified by BLAST-PRODOM'
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/note= "Identified by TMAP, N-terminal domain is
cytoplasmic"
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                                                   in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of CADHP. The CADHP or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. This protein
                                                                                                                                                                 system (acquired immunodeficiency syndrome, thymic dysplasia), neurological (Alzheimer's disease, Parkinson's disease, epilepsy), developmental (renal tubular acidosis, congenital glaucoma) and cell proliferative (cancer, atherosclerosis) disorders. They are also useful
                                                                                                                                                                                                                                  proteins (CADHP). The CADHP polypeptides and polynucleotides are useful in treating, diagnosing and preventing diseases or conditions associated with the decreased expression or overexpression of CADHP, e.g. immune
                                                                                                                                                                                                                                                                                                                                                                                  New human cell adhesion proteins (CADHP) useful for treating, diagnosing and preventing diseases or conditions associated with the aberrant CADHP expression e.g. cancer, acquired immunodeficiency
Sequence
                                                                                                                                                                                                                                                                                            The sequences given
                                                                                                                                                                                                                                                                                                                              Claim 1; Page 115-17; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                 syndrome, Alzheimer's disease and epilepsy
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                                    homology to mouse semaphorin VIa.
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   1017
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Honchell CD,
   AA;
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Burford N,
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Best Local
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37; Conserv
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KPSFVPQTPSVRP 1011
                    KPSFAPLSTSMKP
                                                              PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT--
                                                                                     Conservative
                                                                                                43.5%;
                      67
                                                                                      8;
                                                                                               Score 163.5; DB:
Pred. No. 1.6e-09
                                                                                      Mismatches
                                                                                                          DB 23;
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                                                                                      Indels
                                                                                                           Length 1017;
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ABG79175 standard; Protein; 1032 AA.
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15-NOV-2002 (first entry)

RESULT 15
ABG79175
IID ABG79
XX ABG79
XX ABG79
XX ABG79
XX ABG79
XX Human
XX Human
XX Human
XW Parki
KW Cardi
KW Schiz
KW Immun
KW Janore
KW Viral
KW Viral
KW Viral
KW Janore
KW Janore
KW Viral
KW Janore
KW viral infection; reproductive system disorder; metabolic disturbance; danorexia; wasting disorder; chronic disease; infectious disease; dyslipidaemia; cub; sushi; myelin; von willebrand feat. Human; NOVX; neurodegenerative disease; Alzheimer's disease; anxiety; Parkinson's disease; Huntington's disease; neurological disorder; schizophrenia; manic depression; mental retardation; angina pectoris; schizophrenia; manic depression; mental retardation; angina pectoris; cardiovascular disease; acute heart failure; myocardial infarction; muscular disease; muscular disorder; retinal disease; photoreception; mas proto-oncogene; ribonuclease pancreatic tolloid-like 2; cysteine sulfinic acid decar deafness; keratinisation disorder; cancer; ovarian cancer; melanoma; immunological disorder; inflammatory disease; immune disease; diabet Human semaphorin-like protein #3 semaphorin; serine/threonine protein kinase; precursor; TGF-beta binding; aminotransferase; diabetes;

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Qy
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                                                                                                          Qy
                                                                                                                                                                                                                                                              The present invention relates to new NOVX polypeptides. The polypeptides, CC polypucleotides and antibodies are useful in the manufacture of a CC medicament for treating or preventing neurodegenerative diseases (e.g. Alzhelmer's disease, Parkinson's disease, or Huntington's disease), CC neurological disorders (e.g. anxiety, schizophrenia, manic depression or CC mental retardation), cardiovascular disease (e.g. acute heart failure, CC deafness and diseases (including those involving photoreception, CC deafness and keratinisation disorders), cancer (e.g. ovarian cancer or melanoma), immunological disorders, inflammatory and immune diseases, CC bacterial, fungal, protozoal and viral infections, and reproductive cystem disorders. The proteins of the invention may be used to screen clarge or compounds that modulate the NOVX protein activity or expression, as well as to treat disorders characterised by insufficient or excessive production of NOVX protein or protein forms that have decreased or caberiant activity compared to NOVX wild type protein, such as diabetes, obseity, metabolic disturbances associated with obesity, anorexia and compared siseases and various dyslipidaemias. The nucleic acid contentifying an individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present or content of the invention of a biological sample.
                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                          Query Match
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08-JUN-2001;
29-AUG-2001;
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                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 55; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptides and polynucleotides useful for treating or preventing e.g. neurodegenerative diseases, neurological disorders, cardiovascular diseases, muscular diseases and disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABS64382
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15-MAY-2001;
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1014 KPSFVPQTPSVRP 1026
                                                                         961 PTPTGAKVDYIQ-----
                                    55 KPSFAPLSTSMKP 67
                                                                                              1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPP 54
                                                                                                                                                       37;
                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                 1032 AA;
                                                                                                                                                     Conservative
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2001US-30925BP.
2001US-315639P.
2001US-326393P.
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2001US-291037P.
                                                                                                                                                   43.5%; Score 163.5; DB 23; 50.7%; Pred. No. 1.7e-09; tive 8; Mismatches 15;
                                                                           -GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP 1013
                                                                                                                                                                                          DB 23; Length 1032;
                                                                                                                                                       Indels
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AM, Voss EZ;
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Search completed: September 30, 2003, 16:32:09

Job time : 74 secs

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Database :
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seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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376
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                          Listing first 45 summaries
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/1aa/backfiles1.pep:*
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  US-09-189-035-5
US-09-382-086-5
US-09-513-783A-152
US-09-513-783A-22
US-09-513-783A-22
US-09-513-783A-22
US-09-513-783A-22
US-09-196-270-6
US-08-252-991A-32313
US-09-418-540-5
US-09-252-991A-30563
US-08-252-991A-30563
US-08-252-991A-32720
US-08-252-991A-32720
US-08-933-11721-5
PCT-US-393-703-5
PCT-US-393-11721-5
US-09-252-991A-32385
US-09-252-991A-32385
US-09-066-281B-7
US-09-893-118-7
US-09-893-651-2
US-09-893-651-2
US-09-252-991A-32066
US-08-466-465-6
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                       Sequence 12, Appl
Sequence 30563, Appl
Sequence 30563, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 32720, A
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 1, Appl
Sequence 15, Appl
Sequence 15, Appl
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Sequence 22, Appl
Sequence 32313, A
Sequence 6, Appli
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RESULT 2 US-09-382-086-5 Sequence 5, Application US/09382086 Patent No. 6201106 Patent No. 6201106 GENERAL INFORMATION: APPLICANT: Oue, Henry APPLICANT: Guegler, Warl C. APPLICANT: Guegler, Karl J. APPLICANT: Baughn, Mariah R. TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS FILE REPERENCE: PF-0638 US CURRENT APPLICATION NUMBER: US/09/382,086 CURRENT FILING DATE: 1999-08-24 EARLIER APPLICATION NUMBER: 09/189,035	QY 1 PPPAPQRVDSIQVHSSOPSGQAVTVSROPSLNAYNSLTRSGLKRTPSL Db 264 PTPSSPTIGPAPGSAPGSQYGTMTRQISRHNSTTSSISSGYRRTPSVTAQ QY 51 DVPPKPSFAPLSTSMKP 67 : : : Db 320 HVNGGPLYSQNSISIAP 336	Query Match 19.1%; Score 72; DB 3; Length 480; Best Local Similarity 31.2%; Pred. No. 4.8; Matches 24; Conservative 13; Mismatches 26; Indels 14;	WS-09-189-035-5 Sequence 5, Application US/09189035 Patent No. 6020165 Patent No. 6020165 GENERAL IMPORMATION: APPLICANT: Yue, Henry APPLICANT: Corley, Neil C. APPLICANT: Guegler, Karl J. APPLICANT: Baughn, Mariah R. TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS FILL REFERENCE: PF-0638 US CURRENT APPLICATION NUMBER: US/09/189,035 CURRENT APPLICATION NUMBER: US/09/189,035 CURRENT FILING DATE: 1998-11-10 NUMBER OF SEQ ID NOS: 6 SOFTWARE: PERL PROGRAM SEQ ID NO 5 LENGTH: 480 TYPE: PRT ORGANISM: Homo sapiens FEATURE: - OPHER INFORMATION: 92245671 US-09-189-035-5	ALIGNMENTS	28 64.5 17.2 433 3 US-09-046-158A-2 29 64.5 17.2 897 1 US-07-960-389-2 30 64.5 17.2 1088 4 US-09-233-657-13 31 64.5 17.2 1098 4 US-09-233-657-13 32 64.5 17.2 1099 4 US-08-942-100-2 33 64.5 17.2 1099 4 US-08-966-2 34 64 17.0 641 4 US-09-071-035-456 35 64 17.0 1313 4 US-09-071-035-456 36 64 17.0 1313 4 US-09-071-035-450 37 63.5 16.9 280 4 US-09-252-991A-20783 38 63.5 16.9 280 4 US-09-252-991A-20783 39 63.5 16.9 280 4 US-09-252-991A-20783 40 63 16.8 816 2 US-08-816-693A-53 41 63 16.8 816 3 US-08-885-291-53 42 63 16.8 816 3 US-08-885-291-53 43 62.5 16.6 846 4 US-09-496-672-53 44 62.5 16.5 304 4 US-09-403-343B-22 5 Sequence 5 Sequence 5 Sequence 6 Sequence 7 Sequence 8 Sequence 8 Sequence 9 Sequence
	- A	4			nce 2, Appli nce 2, Appli nce 13, Appli nce 2, Appli nce 2, Appli nce 5, Appli nce 456, App nce 450, App nce 20783, Appli nce 21231, A nce 31291, A ance 32941, A ance 53, Appli nce 53, Appli

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US-08-916-352-2
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                                                                 Matches
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: g2245671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CHIRON CORPORATION
TITLE OF INVENTION: HUMAN POLYHOMEOTITITLE OF INVENTION: TUMOR SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-923-2707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                  TELEPHONE: 510-555-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                              NAME: POTTER, JANE
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/916,352 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                  Local Similarity
                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
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                             2 PPAPORVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTP-SLKPDVPPKPSFAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMERYVILLE
                                                                                                                                                                                                  amino acid
PQPPQVPPTQQVPPSQSQQQAQTLVVQPMLQS-----SPLSLPPDAAPKP---P 493
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                                                                                                                                                                                                                 1004 amino acids
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                                                                 Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     linear
                                                                                                                                                                                 single
                                                                                19.0%;
35.8%;
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                                                                                Score 71.5;
Pred. No. 14;
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US-09-513-783A-22; Sequence 22, Application US/09513783A; Patent No. 6416959;
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US-09-513-783A-152
: Sequence 152, Application US/09513783A
: Patent No. 16416959
: Patent No. 16416959
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                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: EYFP-DEVD-MAP4-EBFP construct US-09-513-783A-22
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SEQ ID NO 22
LENGTH: 161
TYPE: PRT
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                                                                                                                                   Matches
                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A S
FILE REFERENCE: 97-022-
                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/513,783A CURRENT FILING DATE: 2000-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                               862 PSPLENLEQKETPGSQPSEPCSGVSRQEEAKAAVGVTGNDITTPPNKEPPPSPEKKAKPL 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 ATT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 PSPLENLEQKETPGSQPSEPCSGVSRQEEAKAAVGVTGNDITTPPNKEPPPSPEKKAKPL 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 IPIQSKP 500
922 ATT 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 STS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSTSMKP 67
                                 62 STS 64
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18; Conserv
                                                                                                3 PAP-ORVDSIQVHSSOPSGQAVTVSROPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPL 61
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                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giuliano,
                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenneth A.
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                                                                                                                                                   18.5%;
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                                                                                                                                                 Score 69.5;
Pred. No. 41;
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Pred. No. 26;
                                                                                                                                                                   DB 4;
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US-09-252-991A-32313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                            Matches
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SEQ ID NO 32313
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TITLE OF INVENTION: FACTORS
FILE REFERENCE: 50078/004002
CURRENT APPLICATION NUMBER: US/09/196,270
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 60/066,129
EARLIER APPLICATION NUMBER: 60/066,129
EARLIER APPLICATION NUMBER: 60/066,308
EARLIER FILING DATE: 1997-11-21
EARLIER FILING DATE: 1997-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hecht, Peter
APPLICANT: Madden, Kevin
APPLICANT: Fink, Gerald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/066,462
EARLIER FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                            LENGTH: 625
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477 QYAMPHYPSYRAAPSYSSSGCSILPPLQSKIPMLPSRRTMAGGTSLKPNWEFSLNQKSCT 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 PPAPPRLRRLRRGQRAGAPGGDGASAAGCAP-GQAVRIYGAPA----GALPTAG--RAPH 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 LKPDVPPKPSFAPLSTSMKPNDA 70
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                                                                                                                               1 PPPAPQRVDSIQVHSS-----
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                                        -----PSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLS--TSMKPN------DACT 72
                                                                                        PPNAPS~YQSVQGGSSISATANTATYVPVRLAKYPTGPSLTEHLPPLHSNTAGGVFNRQS 476
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                                                                                                                                                                          Score 68.5; DI
Pred. No. 16;
13; Mismatches
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                                                                                                                                                                          27; Indels
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                                                                                                                                                                                                                     Length 625;
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NAME/KEY: Region
LOCATION: 1..1149
OTHER INFORMATION:
US-08-560-005-5
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                                                                                                                                                                                                             US-09-418-540-5
                                                                                                                                                                                                                              RESULT 9
Patent NO. .....

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pot, David A.

APPLICANT: Williams, Lewis T.

APPLICANT: Williams, Lewis T.

APPLICANT: Jefferson, Anne Bennett

APPLICANT: Majerus, Philip W.

APPLICANT: Majerus, Philip W.

APPLICANT: No. 6296848el Grb2 Associating Protein and Nucleic

Three of INVENTION: No. 629684 Bel Grb2 Associating Protein and Nucleic
                                                                                                                                                                   Patent No. 6296848
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, SCITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: Jefferson, Anne Bennett
APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 6001354el Grb2 Associating Protein and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                        880 PPAPPRAAPREEPLITPRIKPEGAPEPEGVAAPPPKNSFNNPAYYVLEGVPHQILPPEPPS 939
                                                                                                                                                                                                                                                                                          940 PARAPVPSATKNKVAIT 956
                                                                                                                                                                                                                                                                                                                                56 PSFAPLSTSMKPNDACT 72
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29.9%;
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Pred. No.
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CORRESPONDENCE ADDRESS:

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US-09-969-528-5; Sequence 5, Application US/09969528; Patent No. 6472197; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415-326-2400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/560,005
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..1149
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 415 TELEPHONE: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
ZIP: 944105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                    APPLICANT: Pot, David A.
Williams, Lewis T.
Jefferson, Anne Bennett
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                         Majerus, Philip W. TITLE OF INVENTION: No. 6472197el Grb2 Associating Protein and Nucleic
                                                                                                                                                                      NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                      940 PARAPVPSATKNKVAIT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           880 PPAPPRAAPREEPLTPRLKPEGAPEPEGVAAPPPKNSFNNPAYYVLEGVPHQLLPPEPPS 939
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                                                                      COUNTRY:
                                                                                   CITY: San Francisco
STATE: California
                                                                                                                       STREET: One Market Plaza, Steuart Tower, Suite 2000
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Pred. No.
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                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,966B
APPLICATION NUMBER: US/08/252,966B
                                                                                                                                                                                               ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                            STATE:
                 NAME: Shelton, Dennis K. REGISTRATION NUMBER: 26,997
                                                                                                                                                                                                                                                                                                             STREET:
REFERENCE/DOCKET NUMBER:
                                                                       CLASSIFICATION:
                                                                                            FILING DATE:
                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                              CITY: Seattle
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/560,005
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ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         880 PPAPPRAAPREEPLTPRLKPEGAPEPEGVAAPPPKNSFNNPAYYVLEGVPHQLLPPEPPS 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 PSFAPLSTSMKPNDACT 72
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08252966B
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                                                                                                                                                                                                                                                                          Washington
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1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                           Hurlin, Peter J. Ayer, Donald E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert N.
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   FHCR17694
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RESULT 12
US-08-252-966B-18
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                                                                                                                                                TELEFAX: (206) 224-077 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ayer, Donald E. TITLE OF INVENTION: Regula TITLE OF INVENTION: Mad or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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MOLECULE TYPE:
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        MOLECULE TYPE: pro
DESCRIPTION: tra
HYPOTHETICAL: YES
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                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FH
TELECOMMUNICATION INFORMATION:
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                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STRANDEDNESS: si
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                                                                                               TYPE:
                                                                                                                                                                                                                                NAME: Shelton, Dennis K. REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 01-JU
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                                                                            STRANDEDNESS:
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                                                                                                               ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   98101-2347
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                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1420 Fifth Ave., Suite 2800
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                                                                                                               1261 amino acids
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                             translation
                                                                              single
                                                                                                                                                                224-0779
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30.7%;
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                             of msina9 cDNA; see Figure 29A,
                                                                                                                                                                                                                    FHCR17694
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-046-585-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 33563
LENGTH: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AND ACID SEQUENCES RELATING TO PSEUDOMONATIFLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08046585 Patent No. 5453362 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30563, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Pseudomonas aeruginosa
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF INVENTION: HOST CELL FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                  APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity tes 23; Conserv
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                                                                                                                   STATE:
                                                                                                                                   STREET: 4
                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAPORVDSIQVHSSQPSGQAVTVSRQPSLNAYNSL-----TRSGLKRTPSLK----
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                                                                                                               CA
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                                                                                                                                     Francisco
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30.7%;
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27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB Pred. No. 4.6;
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RESULT 15
US-08-393-703-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.8%; Score 67; DB Best Local Similarity 32.8%; Pred. No. 1e+C Matches 22; Conservative 10; Mismatches
                                  REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lamarco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: OSMBO, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                 ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: FLEHR, HO!
STREET: 4 Embarcaderc
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EXARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 24-FEE CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1741 PSTVALLESTATESLAPSNTFVAPQPVVVASPAKLOAAATLTEVANGIE-SLGVKPDLPP 1799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 PPAPQRVDSIQVHSSQPSG-----QAVTVSRQPSLNAYNSLTR--SGLKRTPSLKPDVPP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamarco, Kelly
                                                                                                                                                                                                                                              24-FEB-1995
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r~hes 27; Indels
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Job time : 43 secs

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Search completed: September 30, 2003, 16:36:16
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                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                  1741 PSTVALLPSTATESLAPSNTFVAPQPVVVASPAKLQAAATLTEVANGIE-SLGVKPDLPP 1799
                                                                  1800 PPSKAPM 1806
                                                                                                           55 KPSFAPL 61
                                                                                                                                                                                            2 PPAPQRYDSIQVHSSQPSG-----QAVTVSRQPSLNAYNSLTR--SGLKRTPSLKPDVPP 54
                                                                                                                                                                                                                                                                                                                                                                        ESS: single
linear
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OM protein - protein search, using sw model
                                                                                   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: September 30, 2003, 16:22:28; Search time 44 Seconds (without alignments) 157.367 Million cell updates/sec

Title: Perfect score: US-09-856-681-4 376 1 PPPAPQRVDSIQVHSSQPSG......PPXPSFAPLSTSMKPNDACT 72

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1		Query Match 23.1 21.4	Length 961 1322	22 DB	ID A55380 A59288	Description faciogenital dyspl myosin heavy chain hypothetical prote
"L	77	20.5	175	N	T47463	
σı.			744	N	E86255	hypothetical prote
σ.	Çı .		393	Ν	T33103	lin-1 protein
7			494	N	A42170	zinc finger protei
œ ·	5		497	2	JC5076	myc-associated
9	7	19.7	452	N	S22199	imidazoleglycerol-
10	73.5		2282	2	T42717	DNA-binding prote
11	73		867	N	T41308	, μ
12			628	Ν	S01955	cal
13	Ν		657	N	B84869	probable SF16
14			4957	2	T03455	ALR protein -
15	2	19.3	5262	N	T03454	ALR protein
16		•	459	N	A41977	retinoic acid
17	71.5	•	446	2	A42029	transcription
18		19.0	1522	ω	T39371	transcription
19	<u>:</u>	•	2957	N	T33152	hypothetical prote
20	V	•	621	N	JC7278	or prote
21	71	•	1150	N	S58775	mypl protein -
22		•	468	N	T48615	heti
23	70.5	•	1420	N	T37781	
24	V	•	719	N	S62466	probable ATP-depe
25	70	•	747	N	S35546	dent
26	70	•	792	ν		hypothetical prote
27	70	•	1012	N		nous
28	70	•	1201	ν		ro
29	50		ı,	,	~	zinc-finger prote

5	44	43	42	41	40	39	38	37	36	3 5	34	ω ω	32	ω H	30	
67.5	68	68	83	68	68	68	68	68	68	68.5	68.5	68.5	69	69.5	69.5	
18.0	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.2	18.2	18.2	18.4	18.5	18.5	
429	1258	1229	1219	1172	963	736	613	530	428	1188	1106	625	3942	1125	477	
N	N	N	N	N	Ν	Ν	N	N	Н	N	Ŋ	N	N	Ν	Ν	
JC4965	JC5765	A56068	161713	T00065	T40873	T25447	T47975	A45690	TVHUEK	S49915	T31742	S48941	T42730	B41206	A47236	
elkl protein - mou	inositol polyphosp	co-repressor proce	co-repressor prote	hypothetical prote	probable transcrip	hypothetical prote	auxin response fac	transactivator EBN	transforming prote	extensin-like prot	hypothetical prote	regulatory protein	Bassoon protein -	microtubule-associ	zinc-finger protei	

ALIGNMENTS

Query Best	A; Acces A; Statu A; Molec A; Resid A; Cross A; Exper C; Super F; 404-1	C; Acces R; Patel submitt A; Descr A; Refer	RESULT A59288 myosin C;Speci C;Date:	Db	Qy	Qу	Query Best Match	A; Access A; Status A; Moleco A; Resid A; Cross C; Super F; 373-5	R; Paste Cell 79 A; Title A; Refer	RESULT A55380 facioger C;Specio	
Query Match 21.4%; Score 80.5; DB 2; Length 1322; Best Local Similarity 38.4%; Pred. No. 7.4;	A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual type: mRNA A;Residues: 1-1322 <pat> A;Residues: 1-1322 <pat> A;Cross-references: GB:AF209114; PIDN:AAF20150.1 A;Experimental source: strain Sprague-Dawley; clone KP4; cell type type C;Superfamily: myosin motor domain homology <mmo> F;404-1132/Domain: myosin motor domain homology <mmo></mmo></mmo></pat></pat>	C;Accession: A59288 R;Pattel, K.G; Liu, C.; Cameron, P.L.; Cameron, R.S. submitted to GenBank, November 1999 A;Description: Identification of a Novel Mammalian Myosin Class, XVI, A;Reference number: A59288	RESULT 2 A59288 myosin heavy chain Myr 8 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-Sep-	171 PRMPPP 176	62 STSMKP 67	2 PPAPORVDSIQVHSSOPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPL	Query Match 23.1%; Score 87; DB 2; Length 961; Best Local Similarity 34.8%; Pred. No. 1.2; Matches 23; Conservative 5; Mismatches 22; Indels 16; G	A; Accession: ADJOO A; Ratus: preliminary A; Molecule type: mRNA A; Residues: 1-961 <pre>cpas</pre> A; Cross-references: GB:Ul1690; NID:g595424; PID:g595425 A; Cross-references: GB:Ul1690; pleckstrin repeat homology C; Superfamily: CDC24 homology; pleckstrin repeat homology F; 373-561/Domain: CDC24 homology <cd24></cd24>	adle, A.; Logre, L.J.; Follows, M. L.S.; Commune, 994 and characterization of the faciogenital dysplasia A55380; MUID:95042784; PMID:7954831	1 enital dysplasia-associated protein FGD1 - human ies: Homo sapiens (man) : 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 17-Mar ssion: A55380	
	e 1 astrocyte	in Developing	-2000			FAPL 61 : : : LLQM 170	Gaps 2;		>~	-1999 C.E.: Stevenso	

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C;Accession: T47463
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine/proline-rich protein - Arabidopsis thaliana
N,Alternate names: protein T14D3.170
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F20D10.310 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C;Accession: T05646
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A; Introns: 139/2; 675/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cultivar Columbia; BAC clone F20D10 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1111 <BEV>
A; Cross-references: EMBL: AL035538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z15420
A; Accession: T05646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Bevan, M.; Wedler, H.; Kutzner,
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             QΨ
                                                                                                 Q
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                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-175 <JOR>
A;Cross-references: EMBL:AL138649
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z24467
A; Accession: T47463
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                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Columbia; BAC clone T14D3
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             57 SEAPLSTSMKPNDA 70
                                                         27 PAPSPDLADSPLIHASPPS----
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                                                                                                   1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDV----PPKP 56
                                                                                                                                                 20;
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27.0%;
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                                                                                                                                                                      Score 77; DB 2; Pred. No. 1.8;
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Pred. No. 1
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                                                         -KLGSHNSPAESPIEYSSPPEPETEHSPSPSP 76
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                                                                                                                                                                                             Length 175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alogonia, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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                                                                                                                                                                                                                    a;Introns: 94/3; 188/2; 330/1
C;Superfamily: elk-1 transforming
F;26-105/Domain: ets DNA-binding
                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-393 <MIL>
A;Cross-references: EMBL:AF067606; PIDN:AAC17530.1; GSPDB:GN00022; CESP:C37F5.1
A;Experimental source: strain Bristol N2; clone C37F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Miller, N.; Biewald, T. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid C37F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                              A; Gene: lin-1; CESP:C37F5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z21283
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A; Residues: 1-744 <STO>
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                                           151 PPPPPQNPRGNTDFSALSLLGTDSPTTHSVSTPSPTDSVCSPSSSVASSATPSTSSPVDE 210
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  38 TRSGLKRTPSLKPD-----VPPKPSFAPLSTSMKPN 68
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                                                                                       1 PPPAPQR---
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                                                                                                                                                                                                                                           transforming protein; ets DNA-binding domain homology
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                                                                                                                                                        20.1%;
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                                                                                                                                                                                                                         domain homology <ETS>
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Pred. No. 9.6;
                                                                                     --VDSIQVHS-SQPS------GQAVTVSRQPSLNAVNSL 37
                                                                                                                                                             Pred.
                                                                                                                                                                               Score 75.5;
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                                                                                                                                                             No. 6;
                                                                                                                                                                               DB 2; Length 393;
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5

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A;Note: it is uncertain whether Met-18 is the initiator or whether translation is ini R;Bossone, S.A.; Asselin, C.; Patel, A.J.; Marcu, K.B. Proc. Natl. Acad. Sci. U.S.A. 89, 77452-7456, 1992
A;Title: MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating A;Reference number: A46153; MUID:92366479; PMID:1502157
A;Accession: A46153
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Biochemistry 31, 4102-4110, 1992
A;Title: Isolation of a novel cDNA encoding a zinc-finger protein that binds to A;Reference number: A42170; MUID:92232709; PMID:1567856
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F;296-318/Region: zinc finger
F;324-346/Region: zinc finger
F;354-368/Region: zinc finger
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A; Residues: 1-494 < PYR>
                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
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A;Cross-references: DDBJ:D85131; NID:g1752741; PIDN:BAA12728.1; PID:d1013410; PID:g17527 A;Experimental source: pancreatic islet C;Comment: This protein plays a role in the control of transcriptional initiation of gen and between the introns of the mouse gene for immunoglobulin M-D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: HeLa cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-497 <TSU>
                                                                                                                                                                                        A; Accession: JC5076
                                                                                                                                                                                                                 A;Reference number: JC5076; MUID:96428591; PMID:8831693
                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 226, 801-809, 1996
A;Title: Members of the MAZ family: A novel cDNA clone for MAZ from human pancreatic isl
                                                                                                                                                                                                                                                                                                               R;Tsutsui,
                                                                                                                                                                                                                                                                                                                                         C; Accession: JC5076
                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: MAZ protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myc-associated zinc-finger protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;409-430/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;373-405/Region: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 QPPA--PPPPPPPVSAPAAEAAPPASAAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 RTPSLKPDVPPKPSFAPLSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PPPAPQ-----RVDSIQV------HSSQPSGQAVTVSRQPSLNAYNSLTRSGLK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPTPQAPAAEPLQVDLLPVLAAAQESAAAAAAAAAAAAAAVAAAPPAPAAAASTVDTAALK 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRQCRKR--SLSPSTTSSTTAPPPPPQPPTKKGMKPN 245
                                                                                                                                                                                                                                                                                                         Sakatsume, O.; Itakura, K.; Yokoyama, K.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc finger
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C; Keywords: phosphoprotein; zinc finger F;146,204,480/Binding site: phosphate (Ser) (covalent) (by casein kinase II) *status F;349/Binding site: phosphate (Tyr) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) - potato buckeye rot a
C;Species: Phytophthora nicotianae var. parasitica (potato buckeye rot ageni
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 29-Oct-1999
C;Accession: S22199
                                                                                                                                                                                                                                                                                            R:Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Genomics 35, 415-424, 1996
A;Title: The mouse DNA binding protein Rc for the kappa B ew family of large transcriptional proteins.
A;Reference number: Z22238; MUID:97001141; PMID:8812474
A;Accession: T42717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z11591; NID:g3197; PIDN:CAA77675.1; PID:g3198 C;Superfamily: imidazoleglycerol-phosphate dehydratase homology C;Keywords: carbon-oxygen lyase; hydro-lyase F;286-451/Domain: imidazoleglycerol-phosphate dehydratase homology <IPD>
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A;Description: binds V(D)J recombination signal sequence and kappa B motif C;Superfamily: HIV-EP2 enhancer-binding protein C;Keywords: DNA recombination; transcription factor
                                                                                                                                   A;Cross-references: EMBL:L46815; NID:g1377885; PID:g1377886; PIDN:AAB40884.1 A;Experimental source: strain BALB/c; clone T1; thymocyte, brain C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T42717
R;Wu, L.C.; Liu, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: Ig kappa chain gene enhancer Recognition component C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S22199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, January 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Karlovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        멍
                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-2282 <WUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding protein Rc - mouse
                                                                                   C; Function:
                                                                                                            A;Gene: Rc
                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 K 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 ELHRRQPKGMAVVTGR-PRKDCAKFLTTHGIE---DLFPVQIWLEDCPPKPSPEPILLAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 QVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP-----DVPPKPSFAPLSTSM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 RTPSLKPDVPPKPSFAPLSTSMKPNDACT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 K 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PPPAPQ------RVDSIQV------HSSQPSGQAVTVSRQPSLNAYNSLTRSGLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, 2.; Yu, C.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
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19.5%;

Score 73.5;

DB

2;

Length 2282;

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G;Species: Schizosaccharomyces pombe
G;Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 *text_change 02-Sep-2000
G;Accession: T41308
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, submitted to the EMBL Data Library, March 1998
                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S01955
R;MorCh, M.D.; Boyer, J.C.; Haenni, A.L.
Nucleic Acids Res. 16, 6157-6173, 1988
A;Title: Overlapping open reading frames revealed by complete nucleotide sequencing
A;Reference number: S01955; MUID:88289359; PMID:3399388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein, 69K - turnip yellow mosaic virus
C;Species: turnip yellow mosaic virus, TYMV
C;Date: 21-Nov-1993 *sequence_revision 26-May-1995 *text_change 17-Mar-2000
C;Accession: S01955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
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C;Superfamily: GAL4 zinc binuclear cluster homology
F;71-113/Domain: GAL4 zinc binuclear cluster homology <GL4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL022245; PIDN:CAA18305.1; GSPDB:GN00068; SPDB:SPCC320.03 A;Experimental source: strain 972h-; cosmid c320 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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A; Residues: 1-867 < WOO>
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                                               В
                                                                                   Ωy
                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X07441; NID:g62222; PIDN:CAA30321.1; PID:g62223 A;Note: the authors translated the codon ACG for residue 459 as U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SPDB:SPCC320.03
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                                                                                                                                                                                                                                                                                           A; Molecule type:
A; Residues: 1-628
                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                A; Accession: S01955
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                                               119 PPAPQRQHSLPLHITRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 VNSPSLRP 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 MKP 67
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                                                                                                                                                                                                                                                                                        type: genomic RNA
1-628 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PPAPQRVDSI--QVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFA 59
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTVNDRVSNYLPSITSEDSSVTTVPSNSPATLNSYTTSVPSGMSRHEMLMNPSTPEPSLG 388
                                                                                          PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTP----SLKPDV-PPKP
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                                                                                                                                                          Pred.
                                                                                                                                                                                  Score 72.5;
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                                                                                                                                                                                Length 628;
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                                                    REPHHEHARRPDVLPSVP 154
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A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L24.240
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; PID:g2358287 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-657 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable SF16 protein (Helianthus annuus) [imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C;Accession: B84869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Prasad, R.; Zhadano
Oncogene 15, 549-560,
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
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                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-4957 <P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Structure and expression pattern of human ALR, a novel gene with strong hom A;Reference number: Z14954; MUID:97388474; PMID:9247308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T03455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALR protein - human
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nes 25; Conserv
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                                                                                                                                     1925 ELHAKVPSGQPPNFVRSPGTGAFVG-TPSPMRFTFPQAVGEPSLKPPVPQPGLPPPHGIN 1983
                                                    1984 SHFGPGPTLGKP 1995
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                                                                                                                                                                                    12 QVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PPPRPA---SPRVASPRPTSPRVASPRVPSPRA--EVPRTLSPKPPSPRAEVPRSLSPKP 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Y
                                                                                               -SFAPLSTSMKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997
                                                                                                                                                                                                                                                     19.3%;
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Pred. No. 1.8e+02;
Pred. No. 1.8e+02;
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Pred. No. 2
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Length 4957;

Indels

17;

Gaps

-PSLKPDVP----PKP----

56

Length 657;

Indels

13;

Gaps

56

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ALR protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T03454
C;Accession: T03454
R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, a novel gene with strong homolog A;Reference number: Z14954; MUID:97388474; PMID:9247308
A;Accession: T03454
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5262 <PRA>
A;Cross-references: EMBL:AF010403; NID:92358284; PIDN:AAC51734.1; PID:92358285
C;Genetics:
A;Gene: ALR
A;Map possition: 12
C;Superfamily: human ALR protein
C;Keywords: alternative splicing
Search completed: September 30, 2003, 16:35:30 Job time : 55 secs
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                                                                                                                                                                                                                                       2289 SHFGPGPTLGKP 2300
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Database :
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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11. US-09-957-187+85
10. US-09-843-245-3
11. US-10-239-431A-8
12. US-10-239-431A-8
13. US-10-233-950-36
15. US-10-213-950-36
15. US-10-303-683-21
11. US-09-861-683-20
9. US-10-303-683-20
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9. US-10-303-683-20
10. US-09-861-61-34248
15. US-10-177-293-423
16. US-09-854-133-425
17. US-09-864-761-33417
18. US-09-864-761-33417
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     Sequence 21, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 34248, A
Sequence 34248, A
Sequence 300, App
Sequence 425, App
Sequence 425, App
Sequence 425, App
Sequence 33417, A
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                                                                                                                                                                                       Sequence 85, Appl
Sequence 3, Appli
Sequence 20, Appli
Sequence 8, Appli
Sequence 36, Appli
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45	44	43	42	41	40	39	38 8	37	36	3 51	34	33	3 2	31	30	29	28	27	26	25	24	23	22	21			18		16
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17.4	17.4	17.4	17.4	17.4	17.4	17.4		17.6	17.6	17.6	17.7	17.7	18.0	18.0		18.0				•		•			8	8	18.5	9	19.0
1142	473	463	276	261	261	187	144	479	448	200	507	503	5179	5179	5179	405	274	1258	1149	812	697	602	153	729	625	1610	1125	589	360
10	9	14	9	14	14	14	12	9	9	14	14	14	14	10	9	15	15	10	10	15	15	11	10	15	10	15	<u>1</u> 5	9	9
US-09-899-651-2	US-09-864-761-38321	US-10-029-180-80	US-09-864-761-38306	-142	10-062-254-	US-10-062-254-168	US-10-263-828-77	ů	US-09-864-761-44230	US-10-062-254-170	US-10-078-547-24	US-10-078-547-2	US-10-025-380-1068	263	17-1	-10-153-668-	US-10-188-702A-6	US-09-922-543-1	-09-969-5	in	-10-218			5-396-11	801	US-10-100-957A-22	US-10-100-957A-152		US-09-925-301-1116
Sequence 2, Appli	3832	Sequence 80, Appl	Sequence 38306, A	e 142	140		7	Sequence 52/, App	Sequence 44230, A	Sequence 170, App	Sequence 24, Appl	Sequence 2, Appli	Sequence 1068, Ap	Sequence 1068, Ap	Sequence 1068, Ap	Sequence 218, App	Sequence 6, Appli			2	4.				Sequence 294, App	Sequence 22, Appl	မ	N	Sequence 1116, Ap

ALIGNMENTS

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Sequence 85, Application US/09957187

Publication No. US20030054514A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                            ; LENGTH: 1047
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-187-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/957,187
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/123,667
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/234,082
PRIOR APPLICATION NUMBER: 60/234,082
PRIOR APPLICATION NUMBER: 60/234,798
PRIOR APPLICATION NUMBER: 60/233,798
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
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                                                                                                                                                  Best Local Similarity Matches 72; Conserv
                                                                                                                                                                                              Query Match
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PRIOR FILING DATE: 2000-01-04
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LAROChelle, William TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY FILE REFERENCE: 15966-540 CIP
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shimkets, Richard A.
                                                976 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 1035
61 LSTSMKPNDACT 72
                                                                          1 PPPAPORVDSTQVHSSQPSGOAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 60
                                                                                                                                          100.0%; Score 376; DB 11; ilarity 100.0%; Pred. No. 1.9e-29; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                   Length 1047;
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GENERAL INFORMATION:
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LENGTH: 873
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                                                                                                                                                                                                                          SEQ ID NO 20
LENGTH: 374
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TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE
TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN
TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KTNASE
                                                                                  Matches
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/843,245
CURRENT FILING DATE: 2001-04-25
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: McPherson, Peter S. APPLICANT: Ramjaun, Antoine F
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NOIREAUX, VINCENT
APPLICANT: SYKES, CECTLE
TITLE OF INVENTION: PEPTIDE SEQUENCES COMPRISING ONE OR MORE UNITS BINDING
TITLE OF INVENTION: TO PROTEINS OF THE ENA/VASP FAMILY, AND THEIR USES
FILE REFERENCE: 0508-1032
CURRENT APPLICATION NUMBER: US/10/239,431A
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: PCT/FR01/00843
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FRADELIZE, JULIE APPLICANT: FRIEDERICH, EVER APPLICANT: GOLSTEYN, ROY M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: FR 00/03637
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                     ORGANISM: Murine sp.
                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 PPPLPPKPKSISIPQDTHSSEDSNQG-TIKRCPS-----SGSPAKPSHVPPRPPPP 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 RLPPQKPAVLGN 472
208 PPPQPQAKPQVQLH-VQPQAKP-HVQPQP-VSSANTQPRGPLSQAPT-----PAPKFAP 258
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                                                                                  22; Conservative
                                         1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 60
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                                                                                                     21.4%;
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                                                                                  ; Score 80.5; DI
; Pred. No. 2.6;
11; Mismatches
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Pred. No.
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                                                                                                                           DB 12;
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                                                                                                                           Length 374;
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US-10-239-431A-8
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                                                                      US-10-213-990-36
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NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 8
LENGTH: 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10239431A Publication No. US20030170726A1 GENERAL INFORMATION:
                                                                                                                                        NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NOIREAUX, VINCENT
APPLICANT: SYKES, CECILE
TITLE OF INVENTION: PEPTIDE SEQUENCES COMPRISING ONE OR MORE UNITS BINDING
TITLE OF INVENTION: TO PROTEINS OF THE Ena/VASP FAMILY, AND THEIR USES
FILE REFERENCE: 0508-1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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PRIOR APPLICATION NUMBER: FR 00/03637
                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/213,990 CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                               APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
TITLE OF INVENTION: ENZYMES AND METHODS OF USE
FILE REFERENCE: 10182-019-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Murine sp
                                                                                     ORGANISM: Aspergillus
                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 PPPQPQAKPQVQLH-VQPQAKP-HVQPQP-VSSANTQPRGPLSQAPT---
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                                                                                                                           628
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 Conservative
                    19.7%;
                                                                                                                                                                                 2002-08-05
72
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   5; Mismatches
                    Score 74; DB 15;
Pred. No. 22;
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       19;
                                       Length 628;
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       Indels
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       2;
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US-10-303-683-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09291417A Publication No. US20030050230A1
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                               SEQ ID NO 18
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CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: 60/333,378
PRIOR FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: MAP4KS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USIFILE REFERENCE: EX02-126C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Exelixis,
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/291,417A CURRENT FILING DATE: 1999-04-13 EARLIER APPLICATION NUMBER: US 60/081,784 EARLIER FILING DATE: 1998-04-14
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: STE
FILE REFERENCE: 240/300
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MARTINEZ, RICAPPLICANT: WHYTE, DAVID
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                              ORGANISM: Mammalian (Human) KHS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 884
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                                                                                                                                                                                                                                                                 LENGTH: 894
                                                                                                                                                         Local Similarity
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482 RLPP 485
                                                                  432 PPPLPPKPKSIFIPQEMHSTEDENQG-TIKRCP-----
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                               57 SFAP 60
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                                                                                                                                        21;
                                                                                                   1 PPPAPQRVDSI----QVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKP 56
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; Publication No. US20
; GENERAL INFORMATION:
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: MAP4KS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF
FILE REFERENCE: EX02-126C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/333,378 PRIOR FILING DATE: 2001-11-26
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CURRENT FILING DATE: 2002-11-25
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US01/00666 PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                     PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-26
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                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
                                                                                                        APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: FILING DATE: 2001-01
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Pred. No.
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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APPLICANT: Glatt,
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                       TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
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CURRENT FILING DATE:
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Zhao, Xumei
Gannavarpu, Manjula
Kamatkar, Shubhangi
                                                                                                                                                            Sahin, Aysegul
Mills, Gordon B.
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                                                                                                                                                                                                                         Meric, Funda
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Pusztai, Lajos
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Monahan, John
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ilarity 37.5%;
Conservative
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ON: EXPRESSED IN AFTAL LIVER, SIGNAL = 4.8
ON: EXPRESSED IN ADULT LIVER, SIGNAL = 14
ON: EXPRESSED IN PLACENTA, SIGNAL = 7.2
ON: EXPRESSED IN HEART, SIGNAL = 7.2
ON: EXPRESSED IN HEART, SIGNAL = 7.1
ON: EXPRESSED IN HELA, SIGNAL = 7.1
ON: EXPRESSED IN LUNG, SIGNAL = 9.3
ON: EXPRESSED IN HELLA, SIGNAL = 1.2
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   2002-06-21
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Pred. No. 1.3e+02;
9; Mismatches 26;
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                                  ; NAME/KEY: X_region
; LOCATION: (15)..(15)
; OTHER INFORMATION: Xaa =
US-10-259-165-300
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT EILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
                                                                                                                                                              NUMBER OF SEQ ID NOS: 782
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta SEQ ID NO 300
LENGTH: 200
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SEQ ID NO 423
LENGTH: 3664
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Publication No. US20030135888A1
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Query Match
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PRIOR APPLICATION NUMBER: US 60/xxx,xxx
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PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
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TITLE OF INVENTION: GENES THAT ARE MODULATED
FILE REFERENCE: 70030-NP
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                                                                                                                                                  LENGTH: 200
TYPE: PRT
                                                                                                                ORGANISM: Oryza sativa FEATURE:
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Cooper, Bret
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19.4%;
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Pred. No. 1.8e+02;
Score 73;
  DB 12;
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US-09-854-133-425
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                              APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
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CURRENT FILING DATE: 2000-12-14
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                 NUMBER OF SEQ ID NOS: 735
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                               968 SFSRRNSAAPVENCTPLSSVSRP 990
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Kalos, Michael D.
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Elliot, Mark
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o. US20020183499A1
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Pred. No. 2.3e+02;
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; ORGANISM: Homo sapiens US-09-854-133-425
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; Sequence 425, Application US/10144649A
; Publication No. US20030118599A1
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Best Local Similarity
Thehes 27; Conserve
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NUMBER OF SEQ ID NOS: 749
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 425
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              APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENEE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/0180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
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APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C11
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APPLICANT: Wang,
APPLICANT: Fan, I
                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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PRIOR APPLICATION NUMBER: US 09/632,366
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TYPE: PRT
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Wang, ic
Tan, Liqun
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32.5%; Pred. No. 2.3e+02;
ative 11; Mismatches 27;
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FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359

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Search completed: September 30, 2003, 16:43:58
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 41;
OTHER INFORMATION: EXPRESSED IN PRAIN, SIGNAL = 23;
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 25;
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 28;
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 28;
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 46;
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 17;
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 71;
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15;
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 29;
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20;
OTHER INFORMATION: EXPRESSED
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LENGTH: 223
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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Similarity 35.8%;
24; Conservative !
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q8nfy4 homo sapien	Q9p249 homo sapien	Q8nfy5 homo sapien	QBnfy3 homo sapien	Q8nfy6 homo sapien	Q9h9g5 homo sapien	Q9h9k4 homo sapien	Q95ka6 macaca fasc	Q9p2h9 homo sapien	Q9h2e6 homo sapien	Q9eq71 mus musculu	Q96sw4 homo sapien	Q96sm8 homo sapien	Q8nc49 homo sapien	Q96sy4 homo sapien	Q96t04 homo sapien	Description

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ALIGNMENTS

	RESULT Q96T04 ID Q
Older 2001 (Trembliel 19, Created) Older 2001 (Trembliel 19, Last sequence update) Older 2001 (Trembliel 19), Last annotation update) Hypothetical protein FLJ14533. Homo sapiens (Human), Euclieria; Primates; Catarrhini; Hominidae; Homo. NCBL_TaxID=9606; [1] SEQUENCE FROM N.A. Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Ninomiya K., Iwayanagi T.; Namancoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; "NEDO himan cDNA sequencing project."; "Navana Y., Nasahr, Navana Y., Nasahr, Navana Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.; "NEDO himan cDNA sequencing project."; "NEDO himan cDNA sequencing project."; "Navana Y., Saito K., Yamanoto J., Wakamata Y., Nashari Y., Nayana Y., Saito K., Yamamoto J., Wakamata Y., Nashari Y., Nasha	LT 1 04 Q96T04 PRELIMINARY; PRT; 507 AA.

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Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., S
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Te
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Se
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Se
Watanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masul
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masul
Nihomiya K., Iwayanagi T.;
WAEDO human cDNA sequencing project.";
WAEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMEL/GenBank/DDBJ databases.
EMEL, AKO27471; BAB55136.1; -.
InterPro; IPRO33659; Plexin-like.
                                                                                                                                                              Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human cDNA sequencing project."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human)
                                                                                                                  Hypothetical protein SEQUENCE 562 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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  Similarity
72; Conserv
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(TIEMBLICAL 22, Last sequence update)
(TIEMBLICAL 22, Last annotation update)
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
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     Conservative
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                                                                                                               61286 MW;
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Pred. No. 6.3e-33;
           Score 376; Ub -,
No. 6.3e-33;
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     Pred. No. 6. Mismatches
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                                                                                                               708041459E34D78A CRC64;
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Murakawa K., Ono Y., Takiguchi S.,
Ishii S., Kawai Y., Saito K.,
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                                                       Length 562;
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RESULT 5
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.--MAR-2003 (TremBLrel. 23, Last annotat
Hypothetical protein FLJ14748.
Homo sapiens (Human)
Ebkaryota, Metazoa.
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Best Local
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"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027654; BAB55269.1;
InterPro; IPR003659; Plexin-like.
SMART; SM00423; ESI; 1.
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SEQUENCE FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                Hypothetical protein FLJ14595.
Homo sapiens (Human).
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                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 376; DB 4; 100.0%; Pred. No. 6.5e-33;
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RESULT 7
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DT 01-M
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Best Local :
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Q9H2E6;
01-MAR-2001
01-MAR-2001
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Q9EQ71;
01-MAR-2001 (TrEMBLrel. 16, Created)
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                                        Q9H2E6
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20564339; PubMed=10993894;
Klostermann A., Lutz B., Gertler F., Behl C.;
"The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Axon guidance signal
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SMART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                           InterPro; IPR003659; Plexin-like.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1203727;
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                                                                                                                                                                                                                                                                                                                                                            ike Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
r. Biol. Chem. 275:39647-39653(2000).
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                                                                                                    LSTSMKPNDACT 1005
                                                                                                                                                       PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP
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                                        PRELIMINARY;
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Pred. No. 1.2e-32;
; Mismatches 0;
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01-0CT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001627;
Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
Bibl. Chem. 275:39487-39653(2000).
EMBL, AF799656; ARC293781;
InterPro; IPR003659; Plexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20564339; PubMed=1093894;
Klostermann A., Lutz B., Gertler F., Behl C.;
"The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1,/Sema6A-1) bind to the Enabled/Vasodilator-stimulated phosphoprotein-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Semaphora. Human).
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Chara O., "Prediction of the coding sequences of unidentified human genes.XVI The complete sequences of 150 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein KIAA1368 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9Р2Н9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00423; PSI; 1.
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                                                                                                            SEQUENCE
                                                                                                                                                                                    SMART; SM00423; PSI; 1.
SMART; SM00630; Sema; 1.
                                                                                                                                                                                                                                         Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                         Genew; HGNC:10738; SEMA6A.
                                                                                                                                                                                                                                                                                                                                                                   for large proteins in vitro.";
DNA Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                           Hypothetical protein
                                                                                                                                                                                                                                                                                     InterPro; IPR003659; Plexin-like
                                                                                                                                                                                                                                                                                                                                            EMBL; AB037789; BAA92606.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20181126; PubMed=10718198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissu==Brain;
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                                                                                                                                                                                                                                                                    InterPro;
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1 Similarity
72; Conserv
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                                                                                                                                                                                                                                                                    IPR001627;
                                                                                                            1049 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TIEMBLIEL. 15, Created)
(TIEMBLIEL. 15, Last sequence update)
(TIEMBLIEL. 23, Last annotation updat
100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata;
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                                                                                                            116511 MW;
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Pred. No. 1.3e-32;
; Mismatches 0;
Score 376; DB 4;
Pred. No. 1.3e-32;
; Mismatches 0;
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                                                                                                            7781D20ACC7A8AEA CRC64;
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                                                       Length 1049;
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1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAP 60

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RESULT Q5 5 Ka6 1 D 2 T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D T 0 1 D 
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01-MAR-2001
01-MAR-2001
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01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Ninomiya K., Iwayanagi T., Nagahari K., Iwayanagi T., Nagahari K., Iwayanagi T., Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 45.8 kDa protein
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                     Submitted (AUG-2000) to the EMBL; AK022747; BAB14221.1;
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein FLJ12685. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Medulla oblongata;
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.
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                         Hypothetical protein.
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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  49681 MW;
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50.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 163.5;
                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C84BE67EC2F69E2B CRC64;
  EA8BFFFE7067AB04 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 8.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
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RESULT 11
Q9H9G5
     AC DE REPORTE DE RECORDE DE RECOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

ISOGAÍ T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

ISOGAÍ T., Ota T., Hayashi K., Sugano S., Takahashi-Fujii A., Hara H.,

Nishikawa T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO2283; Babi4264.1: -.

EMBL; AKO2283; Babi4264.1: -.

Hypothetical protein.

SEQUENCE 464 AA; 51214 MW; C850600BAESAOC94 CRC64;
"Homo sapiens semaphorin 6D Submitted (JUN-2001) to the EMBL; AF389427; AAM69450.1; InterPro; IPRO01627; Sema. Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-OCT-2002 (TrEMBLrel. 22, Last annotation
Hypothetical protein FLJ12769.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Semaphorin 6D isoform 2.
                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                  Q8NFY6;
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                          SEMA6D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8NFY6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9Н9G5;
                                                                                                                        Qu X., Zhai Y., Wei
                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Н9G5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 KPSFVPQTPSVRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 KPSFAPLSTSMKP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLT-----RSGLKRTPSLKPDVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPSFAPLSTSMKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTPTGAKVDYIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPSFVPQTPSVRP 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPTGAKVDYIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.5%;
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                                                                                                                                                                                                                                                                                                                                                                   22,
22,
23,
                                                                                                                        Yu Y.,
                                                                                                 Y., Tang
isoform
                                                                            EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSLKPDVPP
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Pred. No. 9.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 163.5;
Pred. No. 9.
                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                 F., He F.;
2 (SEMA6D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.7e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                 .2) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                 complete cds.";
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RESULT 13
Q8NFY
AC Q1 X
AC MAMMA
AC TISSU
RA Q1 X
AC MAMMA
AC TISSU
RA Q1 X
AC TISSU
RA AC TISSU
RA CTIS

  RL SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qu X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
"Homo sapiens semaphorin 6D isoform 1 (SEMA6D.1) mRNA, complete cds.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF389430; AAM69453.1; ".
Interpro; IDR001627; Sema.
Pfam; PF01403; Sema; 1.
SMART; SM00330; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBNEY3:
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Semaphorin 6D isoform 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00630; Sema; 1. SEQUENCE 998 AA; 1117
SEQUENCE FROM N.A.
TISSUB-Brain;
Ou X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
Ou X., Wei H., Zhai Y., Yu Y., Tang F., He F.;
"Homo sapiens semaphorin 6D isoform 3 (SEMA6D.3) mRNA, of the Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                   Q8NFY5;
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                       Q8NFY5
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                             Semaphorin 6D isoform 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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Pred. No. 2.4
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Q1-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA1479 (Fragment).
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pfam; pF01403; Sema; 1.
SMART; SM00630; Sema; 1.
SEQUENCE 1017 AA; 113736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
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SMART; SM00630; Sema; 1.
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Pfam; PF01403; Sema;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20277482; PubMed=10819331;
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Pred. No. 2.4e-09;
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OM protein - protein search, using sw model
                                                                                   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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September 30, 2003, 15:15:52; Search time 38 Seconds (without alignments) 89.103 Million cell updates/sec

Title: Perfect score:

Run on:

Sequence: US-09-856-681-4
376
1 PPPAPQRVDSIQVHSSQPSG......PPKPSFAPLSTSMKPNDACT 72

Scoring table: BLOSUM62

Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 127863

127863 seqs, 47026705 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ye semapho panabled/y via a n)00). Hir es of un cDNA cl re axon g re	HUMAN STANDARD; PRT; 1030 AA. SM6A_HUMAN STANDARD; PRT; 1030 AA. O9H2E6; Q9P2H9; 15-SEP-2003 (Rel. 42, Created) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Semaphorin 6A precursor (Semaphorin VIA) (Sema VIA) (Semaphorin 6A-1) (SEMA6A-1). (SEMA6A-1). (SEMA6A OR KIAA1368. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606; [1] SEQUENCE FROM N.A., AND INTERACTION WITH EVL. MEDLINE-20564339; PubMed=10993894; Klostermann A., Lutz B., Gertler F., Behl C.; The orthologous human and murine semaphorin 6A-1 proteins	LT 1

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Best Local
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P98174; Q8N4D9;
01-OCT-1996 (Rel. 34, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
PHATATIVE AND ARC Quanine nucleotide exchange factor (Rho/Rac GEF)
                              MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.
                                                                                                                                                                                                                              Pasteris N.G., Cadle A., Logie L.J., Porteous M.E.M., Schwartz Stevenson R.E., Glover T.W., Wilroy R.S., Gorski J.L.; Stevenson and characterization of the faciogenital dysplasia "Isolation and characterization of the faciogenital dysplasia (Aarskog-Scott syndrome) gene: a putative Rho/Rac guanine nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
VARSPLIC
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                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               TISSUE=Craniofacial;
MEDLINE=95042764; PubMed=7954831;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Mammalia; Euthería; Primates; Catarrhini; Hominidae
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                                                                                                                                      IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00423; PSI; 1.
SMART; SM00630; Sema; 1
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                                                                                                                                                                                               79:669-678(1994).
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                                                                                                                                                                                                                    factor.
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N -> NDISTPLPDNEMSYNTVY
/FTId=VSP_007113.
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No. 1.6e-28;
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Those Matha A. The Jones S. J.M., Marra M.A.;

Thuman and mouse CDNA sequences ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 478:216-220(2000).
-!- FUNCTION: ACTIVATES THE RAS-LIKE FAMILY OF
BY EXCHANGING BOUND GDP FOR FREE GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
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"A mutation in the pleckstrin homology (PH) domain of the FGD1
an Italian family with faciogenital dysplasia (Aarskog-Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orrico A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20389563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20546218; PubMed=11093277; Schwartz C.E., Gillessen-Kaesbach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Two novel mutations confirm FGD1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT AAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT AAS HIS-522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   multisystemic disorder characterized by disproportionately short
stature, and by facial, skeletal, and urogenital anomalies.
SIMILARITY: Contains 1 DBL-homology (DH) domain.
SIMILARITY: Contains 2 PH domains.
SIMILARITY: Contains 1 FYVE-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pancreas and skeletal muscle.
DISEASE: Defects in FGD1 are the cause of Aarskog-Scott stands [MIM:305400]. This factogenital dysplasia is a rare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Expressed in fetal and placenta. Less expressed in liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              responsible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adult heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart,
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brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAC
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Pfam; PF00621; RhoGEF; 1.
SMART; SM00064; FYVE; 1.
SMART; SM00233; PH; 2. Pfam; Pfam; InterPro; IPR001849;
InterPro; IPR000219;
InterPro; IPR000306; GO; GO:0007165; P:signal transd InterPro; IPR001331; GDS_CDC24. HSSP; Q07889; 1AWE. Genew; HGNC:3663; FGD1 GO:0005085; F:guanyl-nucleotide exchange factor activity; GO:0007275; P:development; TAS. GO:0007397; P:histogenesis and organogenesis; TAS. GO:0007165; P:signal transduction; TAS. 305400; PF01363; FYVE; PF00169; PH; 2 RhoGEF. Znf_FYVE. PH.

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ZYX_MOUSE
ID ZYX_MOUSE
AC 06252
DT 01-NO
DT 01-NO
DT 16-NO
DT 16-NO
DT 27Xin
GN MUST
OC BUKAII
OC MARMMA
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZYX_MOUSE
Q62523; P704
Q1-NOV-1997
                                                                                                                                                                                      Otte J., Heischmann A., Breier G., Beckerle M.C., von der Ahe D.; Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

-i- FUNCTION: ADHESION PLAQUE PROTEIN. BINDS ALPHA-ACTININ AND THE CRP PROTEIN. MAY BE A COMPONENT OF A SIGNAL TRANSDUCTION PATHWAY THAT MEDIATES ADHESION-STIMULATED CHANGES IN GENE EXPRESSION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
ZN_FING
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                  Macalma T., Otte J., Hensler M.E., Bockholt S.M., Louis H.A., Kalff-Suske M., Grzeschik K.H., von der Ahe D., Beckerle M.C., "Molecular characterization of human zyxin.", J. Biol. Chem. 271:31470-31478(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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PROSITE; PS00741, DH_1: FALSE_NEG.
PROSITE; PS50010, DH_2: 1.
PROSITE; PS50003; PH_DOMAIN; 2.
PROSITE; PS50178, ZF_FYVE; 1.
                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97094926; PubMed=8940160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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  the European Bioinformatics Institute.
                                                                                             -!- SIMILARITY: Contains 3 LIM zinc-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATES WITH THE ACTIN CYTOSKELETON NEAR THE ADHESION PLAQUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 PRMPPP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P70461;
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5; Mismatches
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Pred. No.
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SH3-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R -> Q (IN AAS).
/FTId=VAR_015237
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FTId=VAR_015236
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There are no
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  restrictions on
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                                                                                                                                                                                                                                                                                                                                    15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mitogen-activated protein kinase kinase kinase kinase 3 (EC 2.7.1.37)
(MAPK/ERK kinase kinase kinase 3) (MEK kinase kinase 3) (MEKKK 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                         germinal center kinase-like kinase.";
J. Biol. Chem. 276:28913-28919(2001).
-!- FUNCTION: May play a role in the
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y07711; CAA68984.1; EMBL; X99063; CAA67510.1;
                       STE20 SUBFAMILY.
-!- SIMILARITY: Contains 1 CNH domain
                                                 MAP4K3-mediated JNK activation.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                         -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- COFACTOR: Magnesium (By similarity).
-!- SUBUNIT: Interacts with SH3GL2. Interaction appears to regulate
                                                                                                                                                                                                         Ramjaun A.R., Angers A., Legendre-Guillemin V.,
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND INTERACTION WITH SH3GL2 MEDLINE=21369947; PubMed=11384986;
                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                              MAP4K3
                                                                                                                                                                                                                                                                                                                                                                                                       Q924I2;
                                                                                                                                                                                                                                                                                                                                                                                                                   M4K3_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00412;
                                                                                                                                                                                          McPherson P.S.;
                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                               Endophilin regulates JNK activation through its interaction with the
                                                                                                                                                                                                                                                                                                                          (Germinal center kinase related protein kinase) (GLK) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                 similarity)
                                                                                                                            Appears to act upstream of the c-jun N-terminal
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435
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LIM 2.
LIM 3.
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Pred. No. 0.4;
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S -> C (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R -> A (IN REF. 1)
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                                                                                                                                         in the response to environmental stress
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell adhesion.
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Pfam; PF00069; pkinase; 1.

Probom; PD000001; Prot_kinase; 1.

SMART; SM00036; CNH; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM002107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ST; FALSE_NEG.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
                                                                                                                                                                                                                                                                                           FGD1_MOUSE
P52734;
                            use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license accordance.
                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative Rho/Rac quanine nucleotide exchange factor (Rho/Rac GEF)
                                                                                                           "Cloning and regional localization dvsplasia (Fqd1) gene.":
                                                                                                                             Pasteris N.G., de
Gorski J.L.;
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                               Eukaryota;
Mammalia; |
                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                     01-OCT-1996
                                                                                                                                                                                                                                                                                                                  MOUSE
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          This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                   MEDLINE=96081343; PubMed=8535076
                                                                                                                                                                                                                                      (Faciogenital dysplasia protein homolog).
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Eutheria;
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IPR000719; Prot_kinase.
IPR002290; Ser_thr_pkinase.
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ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58013AC3B0A3287F CRC64;
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 Bioinformatics
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Best Local
Deloukas P., Matthews I.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clagg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Ellington A.G., Frankland J.A., Griffiths M.N.D., Gwilliam R., Hall R.E.
                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transcription factor GATA-5 (GATA binding fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guanine-nucleotide releasing factor; Zinc-finger; Repeat.

DOMAIN 372 56

DH.

DH.

DOMAIN 7 330

PRO-RICH.

SITE 179 187

SITE 179 187

SH3-BINDING (POTENTIAL).

SOUTH 179 5H3-BINDING (POTENTIAL).

DOMAIN 589 688

DOMAIN 589 FYVE-TYPE.
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InterPro;
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InterPro;
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SMART; SM00064; FYVE; 1.
SMART; SM00233; PH; 2.
SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                       MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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rPro; IPR001849; E
rPro; IPR000219; E
rPro; IPR000306; E
; PF01363; PYVE; 1
; PF01369; PH; 2
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Primates; Catarrhini;
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                   MAZ_HUMAN STANDARD,

P56270; Q15703; Q99443;
P5-7UL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Myc-associated zinc finger protein (MAZI) (Purine-binding
Myc-associated zinc finger protein (MAZI) (Purine-binding
                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kinberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wallis J.M., Walliams L., Williams S.A., Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A., Williams L., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20.";
Nature 414:865-871(2001).
-:- FUNCTION: BINDS TO THE FUNCTIONALLY IMPORTANT CEF-1 NUCLEAR PROTEIN BINDING SITE IN THE CARDIAC-SPECIFIC SLOW/CARDIAC TROPONIC C TRANSCRIPTIONAL ENHANCER. MAY PLAY AN IMPORTANT ROLE IN THE TRANSCRIPTIONAL PROGRAM(S) THAT UNDERLIES SMOOTH MUSCLE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuclear protein.
ZN_FING 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00344; GATA_ZN_FINGER_1; PROSITE; PS50114; GATA_ZN_FINGER_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 2 GATA-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIVERSITY (By similarity). SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL499627; CAC36001.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR00619; GATAZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                              PPPAPQRVDSIQVHSSQP--
                                                                                                                                                                                                                                                                  VCPGPSMAPQASGQE 351
                                                                                                                                                                                                                                                                                                      VPPKPSFAPLSTSMK 66
                                                                                                                                                                                                                                                                                                                                           PRPLAMKKESIQTRKRKPKTIAKARGSSGSTRNASASPSAVASTDSSAATSKAKPSLASP 336
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20.1%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Znf_GATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activator; DNA-binding; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATA-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5DFBA02085695C57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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"Genomic organization and expression of a human gene for Myc-
associated zinc finger protein (MAZ).";

J. Biol. Chem. 273:20603-20614(1998).

-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR WITH DUAL
IN TRANSCRIPTION INITIATION AND TERMINATION. BINDS TO TWO S
MEIAI AND MEIA2, WITHIN THE C-MYC PROMOTER HAVING GREATER
MEIAI AND MEIA2, WITHIN THE C-MYC PROMOTER HAVING GREATER
GO: GO:0006367; P:transcription GO; GO:0006369; P:transcription InterPro; IPR007087; Znf_CZH2. Ffam; PF00096; zf-CZH2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92366479; PubMed=1502157;
Bossone S.A., Asselin C., Patel A.J., Marcu K.B.;
"MAZ, a zinc finger protein, binds to c-MYC and C2 gene sequences regulating transcriptional initiation and termination.";
Proc. Natl. Acad. Sci. U.S.A. 89:7452-7456(1992).
                                                                 MIM;
                                                                                                                                   EMBL; AB017335; BAA33064.1; PIR; A42170; A42170.
                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                  MUSCLE, AND PANCREAS. SEEMS NOT TO BE EXPRESSED IN KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                           AFFINITY FOR THE FORMER. ALSO BINDS TO MULTIPLE G/C-RICH WITHIN THE PROMOTER OF THE SPI FAMILY OF TRANSCRIPTION PI-1- SUBCELLUTAR LOCATION: Nuclear (Probable).
-!- TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LUNG, LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lymphoblastoma;
MEDLINE=98352105; PubN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    responds to MAZ and Sp1.";
J. Biol. Chem. 271:4417-4430(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96224025; Pu
Parks C.L., Shenk T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsutsui H., Sakatsume O., Itakura K., Yokoyama "Members of the MAZ family: a novel cDNA clone pancreatic islet cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92366479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                   Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Song J., Murakami H., Tsutsui H., Tang X., Matsumura M., Kanazawa I., Sun K., Yokoyama K.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pancreatic islets;
MEDLINE=96428591; PubMed=8831693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to two sites within the c-myc promoter."; Biochemistry 31:4102-4110(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Carcinoma;
MEDLINE=92232709;
                                                                                                 TRANSFAC; T00490; -.
TRANSFAC; T02305; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The serotonin la receptor gene contains a TATA-less promoter that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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"Isolation of a novel cDNA encoding a zinc-finger protein that binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. 226:801-809(1996)
                                                                 w; HGNC:6914; MAZ
600999; -.
                                                                                                                                                       M94046; -; NOT_ANNOTATED_CDS.
M93339; -; NOT_ANNOTATED_CDS.
D8513; BAA12728.1; ALT_INIT
U33819; AAB04121.1; ALT_INIT
                                                                                                                                                                                                                                                                                                         non-profit
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                                                                                                                                                                                                                                                                                                         institutions as long as its content
                                 termination from Pol II promoter;
                                                initiation from Pol II promoter; TAS
                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                         Usage
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ZN_FING
ZN_FING
                                         "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                            "Aczonin, a 550-kd putative scaffolding cones. shares homology regions with rim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                       Nagase T., Ishikawa K.-I.,
Nomura N., Ohara O.;
                                                                                                                                                 MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                         TISSUE=Brain
                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                          profilin
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                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99439764; PubMed=10508862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                       SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                          SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-759 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAN STANDARD; PRT; 5147 AA. 043373; 060305; Q9BVCB; Q9UIV2; Q9Y6U9;
                                                                                                                                                                                                                                                                                                                  Biol. 147:151-162(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                        large proteins in 5:31-39(1998).
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PS50157;
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                                                                                                                                                                                                                                   (DEC-1999)
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190 212 C2H2-Type
279 301 C2H2-Type
307 329 C2H2-Type
366 388 C2H2-Type
366 388 C2H2-Type
366 388 C2H2-Type
366 108 POLY-ALA.
133 139 POLY-ALA.
137 161 POLY-ALA.
245 249 POLY-ALA.
245 249 POLY-ALA.
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ZnF_C2H2; 6.
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ZINC_FINGER_C2H2_2;
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25.8%;
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POLY-GLY.
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                                                                                                                         Tanaka A.,
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RA Klausner R.D. (Collins F.S. Nagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hotschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hotschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Ray Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Rahiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butkesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                  EMBL; AB011131;
EMBL; BC001304;
EMBL; AC004082;
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                   MIM;
                                                                                                                                                                                            PIR; T00634; T00634.
HSSP; P04410; 1A25.
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalicki J., Elliott G.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: May act as a scaffolding protein involved in
                                                                                                                               GO; GO:0005856;
                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.L., Feingold E.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 4405-4439 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 4405-5147 FROM N.A.
      GO:0045202;
GO:0005509;
GO:0005544;
GO:0005522;
GO:0007010;
GO:0016080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN:
                                                                                                                                                                                                                                  AC004903; AAD20936.1; -.
AC004886; AAD21789.1; -.
BAD011131; BAA25485.1; -.
BC001304; AAH01304.1; -.
AC004082; AAB97937.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note=No experimental confirmation available; DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Interacts with Rabacl/Pral and SUBCELLULAR LOCATION: Concentrated at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synaptic junctions (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trafficking (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organization of synaptic active zones
                                                                                                                                                   604918;
                                                                                                                                                                                                                                                                                                                                         Y19188; CAB60727.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId-Q9Y6V0-2; Sequence-VSP_003923, VSP_003924, VSP_003927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comment=Additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9Y6V0-1; Sequence=Displayed;
                                                                                                                                                                        HGNC:13406; PCLO
C:cytoskeleton; NAS:
C:synaptic junction; ISS.
F:calcium ton binding activity; ISS.
F:calcium-dependent phospholipid binding acti.
F:profilin binding activity; ISS.
F:profilin binding activity; ISS.
P:cytoskeleton organization and biogenesis; ISS.
P:synaptic vesicle targeting; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoforms
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the presynaptic side of
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                                                                                                                                                                                     _PHYPR
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                           Phytophthora.
NCBI_TaxID=4792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIS7_PHYPR P28624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN
SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phytophthora
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                                                                                                                                                                   SIMILARITY: Belongs to the imidazoleglycerol-phosphate dehydratase
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24, Last sequence up
41, Last annotation
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31.4%;
institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oomycetes;
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K -> KPTDGTKVVSHPITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2 DOMAIN 1.
C2 DOMAIN 2.
S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 X 10 AA TANDEM APPROXIMATE REPEATS A-K-P-Q-P-Q-Q-P-X. C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2).
/FTId=VSP_003927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_003925.
TAHKS -> SKRRK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VSP_003926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> KPTDGTKVVSHPITGEIQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> GQVMVVQNAS (in isoform 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M4K3_HUMAN STANDARD; PRT; 894 AA.

ØBIVHB; Q&IVHT; Q&UDMS; QQYGRS;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
M1togen-activated protein kinase kinase kinase 3

(MAPK/ERK kinase kinase kinase 3) (MEK kinase kinase 3)
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS GORRY M.C., Zhang Y., Marks J Pallos D., Hart T.C.; "Physical/genetic map of the Submitted (NOV-2001) to the F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO1548; HAD-SF-IA-hyp1; 1.
TIGRFAMS; TIGRO1556; Histidinol-ppas; 1.
PROSITE; PS00954; IGP_DEHYDRATASE_1; 1.
PROSITE; PS00955; IGP_DEHYDRATASE_2; 1.
PROSITE; PS00955; IGP_DEHYDRATASE_2; 1.
PROSITE; PS00955; IGP_DEHYDRATASE_3; 1.
POWATURE PROSITE PROS
                                                                                                  Edwards J., Wohldmann P., Hawkins M., Harkins Submitted (JUN-1999) to the EMBL/GenBank/DDBJ-i-FUNCTION: May play a role in the response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Macrophage, and Skeletal muscle; MEDLINE=97420743; PubMed=9275185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00702; Hydrolase; 1. Pfam; PF00475; IGPD; 1. ProDom; PD002282; IGPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Activation of the c-Jun N-terminal kinase pathway kinase related to human germinal center kinase."; Proc. Natl. Acad. Sci. U.S.A. 94:9687-9692(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2), FUNCTION, MUTAGENESIS OF LYS-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tan T.-H., Yao Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diener K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                       SEQUENCE OF 1-712 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000807; IGPD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Germinal center kinase related protein kinase) (GLK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
pathway.
CATALYTIC ACTIVITY:
                                                                  Appears to act upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 QVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKP------DVPPKPSFAPLSTSM
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21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang X.S., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 AA;
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                                                                                                                                                                                                                                                                                                                                                                     Y., Marks J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452
                                                                                                                                                                                                                                                                                                                                                                                                        (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.7%;
34.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase.
       ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        С.,
                                                                                                                                                                                                    (ISOFORM 1)
                                                                                                                                                                                                                                                                          9 2p22-2p21 region
EMBL/GenBank/DDBJ
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                                                                      the c-jun
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       protein
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ne c-jun N-terminal
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                                                                                                                                                                                                                                                                                                                                                                        Hart S., Cortelli J.,
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                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zukowski M.,
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use
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                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STE20 SUBFAMILY.
SIMILARITY: Contains 1 CNH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: Ubiquitously expressed in all tissues examined, with high levels in heart, brain, placenta, skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoprotein.
COFACTOR: Magnesium.
SUBUNIT: Interacts w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 muscle, kidney and pancreas and lower levels in lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Interacts with SH3GL2. Interaction appears to regulate MAP4K3-mediated JNK activation (By similarity). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isoforms-3;
        AF445401

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Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q8IVH8-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note=No experimental confirmation available;
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                                                                                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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RESULT 11
PCLO.RAT
ID PCLO.
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DT 28-
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                                                                                                                               PCLO_RAT STANDARD; PRT; 5085 AA.

09JKS6; 09JLT1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FCOLO protein (Multidomain presynaptic cytomatrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
BINDING
ACT_SITE
                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001245; Tyr_p
Pfam; PF00780; CNH; 1.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; FALSE_NEG
PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00036; CNH; 1.
SMART; SM00220; S_TKC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 604921
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                                                                                                                                                                                                                                                                                                                               482
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AF445409;
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AF445405;
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AF445401;
AF445402;
AF445403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD000001; Prot_kinase;
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48 48
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AAN75850.1;
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32.8%;
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Ser_thr_pkinase.
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JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 1; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNPGFDLSRRNP -> MA (in isoform /FTId=VSP_007052.
Missing (in isoform 3).
/FTId=VSP_007053.
K->E: LOSS OF KINASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO ACTIVATE JNK FAMILY.
N -> D (IN REF. 1; AAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> D (IN REF. 1; AAC15472).
6EB77BBB34E5B733 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                   protein)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        481
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SEQUENCE FROM N.A. NCBI_TaxID=10116;

(ISOFORM

2),

AND

INTERACTION WITH RABACI

Eutheria;

Craniata; Vert Sciurognathi;

Vertebrata; Muridae;

Euteleostomi;

Murinae;

Rattus.

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R GO; GO:0045202; C:synaptic junction; IDA.
R GO; GO:0045202; C:synaptic junction; IDA.
R GO; GO:0005509; F:calcium ion binding activity; IDA.
R GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . .; R GO; GO:0005544; F:calcium-dependent phospholipid binding acti. . .; R GO; GO:0005010; P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization and biogenesis; ISS.
R GO; GO:0016080; C2.
P:cytoskeleton organization an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04410; 1A25.

G0; G0:004520; C:s9;

G0; G0:0005509; F:ca

G0; G0:0005544; F:ca

G0; G0:0005522; F:pp

G0; G0:0007010; P:cy

G0; G0:0016080; P:cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;
Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;
Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;
The unusual C(2)-domain in the active-zone protein piccolo:
Implications for Ca(2+) regulation of neurotransmitter release.";
EMBO J. 20:1605-1619(2001).

IF FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).

Interacts with Rabacl/Pral and profilin.
                                                                             ZN_FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
  DOMAIN
                                                       DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                    Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).

Fenster S.D., Cases-Langhoff C., Gundelfinger Submitted (JAN-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fenster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B., Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.; "Piccolo, a presynaptic zinc finger protein structurally related to bassoon.";
                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674; VAL-4688; MET-4689; VAL-4690; SER-4691; GLN-4692; ASN-4693 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 25:203-214(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21181819;    PubMed=11285225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specificity and induces a large conformational change. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: C2 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )unctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF138789;
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                                                                                                                                                                                                              Alternative
  523
1010
2351
4442
4653
4968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF07822.2; -.
AAF63196.1; -.
                              547
1033
2362
4536
4752
                                                                                                                                                                                                           splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_003930, VSP_003931;
1 is involved in binding calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing; Named isoforms=2;
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                                                                       P-A-K-P-Q-P-Q-Q-P-X.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
POLY-PRO.
PDZ.
C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                     12 X 10 AA TANDEM APPROXIMATE REPEATS OF
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RESULT 12
V70K_TYMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                  Morch M.D., Boyer J.C., Haenni A.L.; "Overlapping open reading frames revealed by complete nucleotide sequencing of turnip yellow mosaic virus genomic RNA."; Nucleic Acids Res. 16:6157-6173(1988).
                                                                                                                                                                                                                                                                                                     69 kDa protein.
Turnip yellow mosaic virus.
Viruses; ssrNa positive-strand viruses, no DNA stage; Tymovirus.
                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel.
01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
SEQUENCE
                                     EMBL; x07441; CAA30321.1; ALT_SEQ. PIR; S01955; S01955.
                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   use by non-profit institumodified and this statement
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                          Nucleic Acids Res. 16:6.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=88289359; PubMed=3399388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
InterPro; IPR004935; Tymo_45_70kDa.
Pfam; PF03251; Tymo_45kd_70kd; 1.
SEQUENCE 628 AA; 69195 MW; 9B01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=12154;
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.5%;
26.4%;
                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                           Last
                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND CALCIUM-DEPENDENT PHOSPHOLIPID BINDING ACTIVITY.
D->A: COMPLETE LOSS OF CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 73.5;
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M->S: INCREASED AFFINITY FOR CALCIUM. VV->SS: 10-FOLD INCREASE IN AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A->S: NO EFFECT ON CALCIUM-BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QN->AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D->A: COMPLETE LOSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKPTN -> SKRRK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VM->SS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VSP_003930
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
 9B01CE5ADFCEAC77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5A1BB543201A7450 CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODERATE INCREASE IN AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FOLD INCREASE IN AFFINITY FOR
                                                                                                                                                                                                                                                                                                                                                                                                628 AA
                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                   Usage
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                                                                                                               its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                     and for
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                                                                                                                                           a collaboration
MBL outstation -
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Query Match Best Local Similarity

19.3%; 29.6%;

Score 72.5; I Pred. No. 9.8;

DΒ

Length 628;

97

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VQ
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                              Query Match
Best Local
                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                     MOI. Cell. Biol. 12:817-827(1992).

11- FUNCTION: POSITIVE-ACTING RANSCRIPTION FACTOR THAT BINDS TO THE IMMUNOCLOBULIN ENCHANCER MUES MOTIF. IT BINDS ALSO VERY WELL TO A USF/MLTF SITE. BINDING OF TFE3 TO DNA INDUCES DNA BENDING.

15- SUBUNIT: Efficient DNA binding requires dimerization with another
                                                                                                                   PROSITE; PS00038; HLH_1; 1.

PROSITE; PS50888; HLH_2; 1.

Transcription regulation; DNA-binding; Activator; Nuclear protein.

NON_TER 1
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence up 30-MAY-2000 (Rel. 39, Last annotation Transcription factor E3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                            SEQUENCE
                                                                     DOMAIN
                                                                              DOMAIN
                                                                                       DNA_BIND
                                                                                                           DOMAIN
                                                                                                                                                           SMART; SM00353;
                                                                                                                                                                   Pfam; PF00010; HLH; 1.
                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                 "mTPE3, an X-linked transcriptional activator containing basic helix-loop-helix and zipper domains, utilizes the zipper to stabilize both DNA binding and multimerization.";
Mol. Cell. Biol. 12:817-827(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q64092;
01-NOV-1997
                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                   EMBL; S76673; AAB21130.1;
                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92123207; PubMed-1732746;
Roman C., Matera A.G., Cooper C., Artandi S., Blain S., Ward D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFE3 OR TCFE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFE3_MOUSE
                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                  BHLH protein
                                                                                                                                                                             MGI:98511; Tcfe
rPro; IPR001092;
                                                                                                                                                                                                          A42029; A42029.
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                    22;
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                            Similarity
PPPA--PQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSF 58
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                    Conservative
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233
282
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                                                                     232
273
303
                                                                                                          144
                                                            47891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
                           19.0%;
34.4%;
                                                                                                                                                                             HLH_basic
                   9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                 Pred. No. 8.4;
9; Mismatches
                                                        HELIX-LOOP-HELIX MOTIF (BY SIMILARITY)
LEUCINE-ZIPPER (POTENTIAL)
; 79115373AD7F131E CRC64;
                                       Score
                                                                                      BASIC DOMAL
                                                                                                          STRONG TRANSCRIPTION ACTIVATION DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                              No. 8
                                                                                       DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446
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                                       DB 1;
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                    28;
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                                       Length 446;
                   Indels 5;
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   RESULT 14
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28-FEB-2003
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                  REPEAT
REPEAT
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DOMAIN
                                                                   REPEAT
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                                                                                                          REPEAT
                                                                                                                                       LIM domain;
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                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00478; LIM_DOMAIN_1; PROSITE; PS50023; LIM_DOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00132; LIM;
                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000094; LIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF045941; AAC78461.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Champliaud M.-F., Burgeson R.E., Jin W., Baden H.P., Olson P.F.; "CDNA cloning and characterization of sciellin, a LIM domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99030435; PubMed=9813070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Foreskin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the keratinocyte cornified envelope.";
Biol. Chem. 273:31547-31554(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005737;
GO:0008544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed in keratinocytes, amniotic tissue, fores) spinosum and stratum granulosum, hair follicle and SIMILARITY: Contains 1 LIM zinc-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homotypic or heterotypic associations and may funct sciellin to the cornified envelope.
SUBCELLULAR LOCATION: Cytoplasmic. May become cross membrane proteins by transglutaminase.
TISSUE SPECIFICITY: Highly expressed in esophagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: May function in the assembly or regulation of p in the cornified envelope. The LIM domain may be involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 AQPL 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGNC:10573; SCEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001781;
                                                                                                                                                                                                                                                                                                                   Metal-binding; Zinc;
599
2311
2311
2247
2267
2267
2287
327
327
327
327
327
327
347
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427
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P:epidermal differentiation; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:cytoplasm;
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                                                                                                                                                                                                                                                                        X APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                              FALSE_NEG
                                                                                                                                                                                                                                                                                                                Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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RC TISSUB-Lung, and Lymph;

RC TISSUB-Lung, and Lymph;

RX MEDIXINE-2388257; PubMed=12477932;

RX MEDIXINE-2388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Fahey J., Halton E., Ketteman M., Madan A., Sanchez A.,

Green E.D., Dickson M.C.,
PHODO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
"Generation and sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Involved in the regulation of Hox gene expression a
segment specification during paraxial mesoderm and neural cre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gunster M.J., Satijn D.P., Hamer K.M., den Blaauwen J.L., de Bruijn D., Alkema M.J., van Lohuizen M., van Driel R., Ot "Identification and characterization of interactions between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P78364: Q9WVM3; Q9BU63;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vertebrate polycomb-group protein BMI1 and human homologs of
polyhomeotic.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND INTERACTION WITH BMI1. MEDILINE-97220024; PubMed=9121482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHC1 OR EDR1 OR PH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyhomeotic-like protein 1 (Early development regulator protein 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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             development (By similarity).
SUBUNIT: Homodimer. Interacts with BMI1.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biol. 17:2326-2335(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SIQVHSSQPSGQ-----AVTVSRQ----PSLNAYNSLTRSGL-KRTPSL
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| HPPIPPKPS-SPVSS---PN 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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30.0%;
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Pred. No. 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.
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                                                                                                                                             Hox gene expression and esoderm and neural crest
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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494 IPIQSKP 500
                                                                                                           448 PQPPQVPPTQQVPPSQSQQQAQTLVVQPMLQS-----SPLSLPPDAAPKP---P
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BC002871; AAH02871.1; ALT_INIT.
BC017748; AAH17748.1; ALT_INIT.
                                                        61 LSTSMKP 67
                                                                                                                                                           2 PPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTP-SLKPDVPPKPSFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00454;
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HL -> LK (IN REF. 1).

S -> T (IN REF. 1).

A -> T (IN REF. 1).

V -> G (IN REF. 1).

L -> F (IN REF. 1).

L -> F (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                         MW.
                                                                                                                                                                                                                                                     Score 71.5;
Pred. No. 21;
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                                                                                                                                                                                                                          Mismatches
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> F (IN REF. 1).
> F (IN REF. 1).
5E35765758904C4F CRC64;
                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                             Length 1004;
                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                       Gaps
                                                                                                              493
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Search completed: September 30, 2003, 16:33:00 Job time : 40 secs